

RESULT 2
US-08-179-574-1
Sequence 1, Application US/08179574
; Patent No. 5506097
GENERAL INFORMATION:
APPLICANT: Huntington Potter
TITLE OF INVENTION: Compounds and Methods for Inhibiting
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADRESSEE: Usamah Kayyal
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,574
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 07/819,361
APPLICATION NUMBER: 13-JAN-1992
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU90-03A3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-179-574-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGATIGLMGVVIA 42
Db 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGATIGLMGVVIA 42

RESULT 3
US-08-147-144-1
Sequence 1, Application US/08347144
; Patent No. 5589154
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
CORRESPONDENCE ADDRESS:
ADRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,144
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: AUBRECHT, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: AMYLOID PEPTIDE
US-08-347-144-1

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGATIGLMGVVIA 42
Db 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGATIGLMGVVIA 42

RESULT 4
US-08-462-859A-19
sequence-49-Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobson, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
Title of Invention: Using Same to Access Agents Which Down Regulate Formation
Number of Sequences: 19
Title of Invention: of B-Amyloid Peptide
Correspondence Address:
Addressee: American Cyanamid Company
Street: One Cyanamid Plaza
City: Wayne
State: New Jersey
Country: United States
Zip: 07470-8426
Computer Readable Form:
Medium Type: Floppy disk
Computer: IBM PC compatible
Operating System: PC DOS/MS-DOS
Software: PatentIn Release #1.0, Version #1.30
Current Application Data:
Application Number: US/08/462,859A
Filing Date: 05-JUN-1995
Classification: 435
Attorney/Agent Information:
Name: Barnhard, Elizabeth M.
Registration Number: 31,088
Reference/Docket Number: 31,844-04
Telecommunication Information:
Telephone: (201)831-3246
Telex: (201)831-3305
Information for Seq ID No: 19:
Sequence Characteristics:
Length: 42 amino acids
Type: amino acid
Strandness:
Topology: linear
Molecule Type: protein
US-08-462-859A-19

Query Match 100.0%; Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

STREET: One Campus Drive
 CITY: Parsippany
 STATE: New Jersey
 COUNTY: United States
 ZIP: 07054

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,247A
 FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Barnhard, Elizabeth M.
 PATENT NO.: 5693477

TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of Using Same to Access Agents Which Down-Regulate Formation of B-Amyloid Peptide

TITLE OF INVENTION: Of Sequences: 19

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Anne Rosenblum
 STREET: 163 Delaware Avenue, Suite 212
 CITY: Delmar
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 12054

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/123,659A
 FILING DATE: 20-SEP-1993
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Rosenblum, Anne M.
 REGISTRATION NUMBER: 30,419
 REFERENCE/DOCKET NUMBER: 31,844-01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (518)475-0611
 TELEFAX: (518)475-0619

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-123-659A-19

RESULT 5

Sequence T9—Application US/08123659A

GENERAL INFORMATION:
 APPLICANT: Jacobson, J. S.
 PATENT NO.: 5693478

TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of Using Same to Access Agents Which Down-Regulate Formation of B-Amyloid Peptide

TITLE OF INVENTION: Of Sequences: 19

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTY: United States
 ZIP: 07470-8426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,248A
 FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Barnhard, Elizabeth M.
 PATENT NO.: 5693478

TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of Using Same to Access Agents Which Down-Regulate Formation of B-Amyloid Peptide

TITLE OF INVENTION: Of Sequences: 19

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company

US-08-464-247A-19

RESULT 6

Sequence T9—Application US/08464247A

GENERAL INFORMATION:
 APPLICANT: Vittek, M. P.

TITLE OF INVENTION: No. 5653478el Amyloid Precursor and Method of Using Same to Access Agents Which Down-Regulate Formation of B-Amyloid Peptide

TITLE OF INVENTION: Of Sequences: 19

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-464-248A-19

Query Match Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 8

US-08-476-464A-1

Sequence 1, Application US/08476464A
Patent No. 5707821.

GENERAL INFORMATION:
APPLICANT: RUDEL, RUSSELL E.
ADDRESS: TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION INFORMATION:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REFERENCE/DOCKET NUMBER: 152270-0-02300
TELEPHONE: (415)576-2400
TELEFAX: (415)576-0300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-476-464A-1

Query Match Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 9

US-08-304-585-2

Sequence 2, Application US/08304585
Patent No. 5721106

GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mandy, Patrick W.
TITLE OF INVENTION: LABELLED BETA AMYLOID PEPTIDE AND METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muettig, Raasch, Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Muettig, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 11.0.00010120

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: not relevant

US-08-304-585-2

Query Match Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 10

US-08-302-808-5

Sequence 5, Application US/08302808
Patent No. 575349

GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Ichiko

TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR DERIVATIVES AND USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIVE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
ZIP: 02019

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastaEQ Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994

CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24 JAN 1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286385/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-302-808-5

RESULT 11
US-08-268-348A-1
; Sequence 1, Application US/08268348A
; Patent No. 5750374
; GENERAL INFORMATION:
; APPLICANT: Dobeli, Heinz
; APPLICANT: Dreger, Nicholas
; APPLICANT: Trottman, Gerda H
; APPLICANT: Jakob, Peter
; APPLICANT: Stüber, Dietrich
; TITLE OF INVENTION: Process for Producing Hydrophobic
; TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
; TITLE OF INVENTION: Producing Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/268348A
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parise, John P.
; REGISTRATION NUMBER: 34,403
; REFERENCE/DOCKET NUMBER: 4105/157
; TELEPHONE: (201) 235-6326
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: N-terminal
; US-08-268-348A-1

Query Match Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
US-08-433-734-2
; Sequence 2, Application US/08433734
; Patent No. 537773
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyn, Patrick W.
; APPLICANT: Manganaro, John E.
; TITLE OF INVENTION: Labelled Peptide and Methods
; for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; STATE: MN
; CITY: Minneapolis
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,734
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1220
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-734-2

Query Match Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMGGVIA 42

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMGGVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMGGVIA 42

RESULT 13
US-08-609-090-9
Sequence 9, Application US/08609090
Patent No. 5840838

GENERAL INFORMATION:

APPLICANT: HENSLEY, Kenneth
ADDRESS: 1000 N. 10TH ST.
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19107

CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

COMPUTER: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear

MOLECULE TYPE: peptide

US-08-609-090-9

Query Match Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0

GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY NEUROTOXIN INHIBITORS (AS AMENDED)

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

RESULT 14
US-07-737-371E-72
Sequence 72, Application US/07737371E

Patent No. 5876948

GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY NEUROTOXIN INHIBITORS (AS AMENDED)

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

Query Match Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0

GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY NEUROTOXIN INHIBITORS (AS AMENDED)

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

Query Match Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0

GENERAL INFORMATION:

APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY NEUROTOXIN INHIBITORS (AS AMENDED)

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-422-333-4

Query Match 100.0%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMYGGVVA 42
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMYGGVVA 42

Search completed: April 21, 2003, 12:08:07
Job time : 16 secs



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:06:50 ; Search time 15 Seconds
(without alignments)
211.719 Million cell updates/sec

Title: US-09-580-018-42

Perfect-score: 217

Sequence: 1 DAEFRHDSGYEVHKLVFF...DVGNSKGAIIGLMVGGVVIA 42

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen Parameters : 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA: *

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2: /cgn2_6/ptodata/2/pubpaas/us06_new_pub_pep:*

3: /cgn2_6/ptodata/2/pubpaas/us06_new_pub_pep:*

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6: /cgn2_6/ptodata/2/pubpaas/us07_pubcomb_pep:*

7: /cgn2_6/ptodata/2/pubpaas/pctns_pubcomb_pep:*

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12: /cgn2_6/ptodata/2/pubpaas/us10_pubcomb_pep:*

13: /cgn2_6/ptodata/2/pubpaas/us60_new_pub_pep:*

14: /cgn2_6/ptodata/2/pubpaas/us60_pubcomb_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Query	Score	Match	Length	DB	ID	Description
1	217	100.0	42	8	US-08-923-055-2	Sequence 2, Appli	Sequence 2, Appli
2	217	100.0	42	9	US-10-051-496-2	Sequence 2, Appli	Sequence 2, Appli
3	217	100.0	42	9	US-10-082-004-7	Sequence 7, Appli	Sequence 7, Appli
4	217	100.0	42	9	US-09-962-055C-37	Sequence 37, Appli	Sequence 37, Appli
5	217	100.0	42	9	US-09-848-516-14	Sequence 174, App	Sequence 174, App
6	217	100.0	42	9	US-09-865-294-65	Sequence 65, Appli	Sequence 65, Appli
7	217	100.0	42	10	US-09-867-847-1	Sequence 1, Appli	Sequence 1, Appli
8	217	100.0	42	10	US-09-956-625-26	Sequence 26, Appli	Sequence 26, Appli
9	217	100.0	42	10	US-09-731-460-1	Sequence 1, Appli	Sequence 1, Appli
10	217	100.0	43	9	US-10-076-108-7	Sequence 7, Appli	Sequence 7, Appli
11	217	100.0	43	9	US-10-051-496-1	Sequence 1, Appli	Sequence 1, Appli
12	217	100.0	43	9	US-10-217-459-1	Sequence 1, Appli	Sequence 1, Appli
13	217	100.0	43	10	US-09-280-966-1	Sequence 1, Appli	Sequence 1, Appli
14	217	100.0	43	10	US-09-904-987-1	Sequence 1, Appli	Sequence 1, Appli
15	217	100.0	43	10	US-09-808-037-3	Sequence 3, Appli	Sequence 3, Appli
16	217	100.0	43	10	US-08-866-712-3	Sequence 3, Appli	Sequence 3, Appli
17	217	100.0	43	10	US-09-972-475-1	Sequence 1, Appli	Sequence 1, Appli
18	217	100.0	43	10	US-09-992-800-1	Sequence 1, Appli	Sequence 1, Appli
19	217	100.0	43	10	US-09-895-443-1	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-923-055-2

; Sequence 2, Application US/08923055
; Patent No. US200101001327A1
; GENERAL INFORMATION:
; APPLICANT: Dana Giulian
; TITLE OF INVENTION: Identification of Agents that Protect
; Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,055
FILING DATE: Sept - 03 -97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Bearrell
REGISTRATION NUMBER: 34-293
REFERENCE/DOCKET NUMBER: BYLR-0038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-923-055-2 Query Match 100.0% ; Score 217; DB 8; Length 42;
 Best Local Similarity 100.0% ; Pred. No. 1.5e-22; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMVGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMVGGVIA 42

RESULT 2
 ; Sequence 2, Application US/10051496-2
 ; Publication No. US200018260A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kei-Lai L. Fong
 ; TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for
 ; Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-39)
 ; ABETAS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kei-Lai L. Fong
 ; STREET: 1004 West 8th Avenue
 ; CITY: King of Prussia
 ; STATE: Pennsylvania
 ; COUNTY: USA
 ; ZIP: 19406
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.50 inch, 1.44MB storage
 ; COMPUTER: IBM PC Compatibles
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: MS No. US/0020182660A1epad

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/051,496
 FILING DATE: 18-Jan-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/784,854 A
 FILING DATE: 16-Feb-2001
 APPLICATION NUMBER: 60/183,407
 FILING DATE: 18-February 2000
 ATTORNEY/AGENT INFORMATION:
 NAME: Koenig, C. Frederick III
 REGISTRATION NUMBER: 29,662
 REFERENCE/DOCKET NUMBER: PBI-PT001.1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-6400
 TELEFAX: (215) 568-6400

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 Amino Acid
 TYPE: Amino Acid
 TOPOLOGY: Linear
 MOLECULE TYPE: Protein

FEATURE:
 NAME/KEY: Signal Sequence
 LOCATION: 1-42
 IDENTIFICATION METHOD: Similarity to other sequences, hydro-phobic
 OTHER INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1-42
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-051-496-2 Query Match 100.0% ; Score 217; DB 9; Length 42;

Best Local Similarity 100.0% ; Pred. No. 1.5e-22; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMVGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMVGGVIA 42

RESULT 3
 US-10-082-804-7
 ; Sequence 7, Application US/10082804
 ; Publication No. US20020194632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McConlogue, Lisa
 ; ATTORNEY: Gurney, Mark E.
 ; TITLE OF INVENTION: Transgenic Knockouts of BACE-1
 ; FILE REFERENCE: MBHB 02-329-A
 ; CURRENT APPLICATION NUMBER: US/10/082,804
 ; CURRENT FILING DATE: 2002-02-22
 ; PRIOR APPLICATION NUMBER: 60/271,092
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: 60/271,514
 ; PRIOR FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 60/293,762
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: A-beta 42 sequence.
 US-10-082-804-7
 ; Query Match 100.0% ; Score 217; DB 9; Length 42;
 ; Best Local Similarity 100.0% ; Pred. No. 1.5e-22;
 ; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMVGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMVGGVIA 42

RESULT 4
 US-09-902-955C-37
 ; Sequence 37, Application US/09/62955C
 ; Publication No. US20030013648A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerardo M. Castillo
 ; APPLICANT: Alan D. Show
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrick M. Dwyer
 ; STREET: ProteoTech, Inc., 1818 Westlake Avenue N, Suite 114
 ; CITY: Seattle
 ; STATE: WA (Washington)
 ; COUNTRY: United States of America
 ; ZIP: 98109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: Windows 98
 ; SOFTWARE: Wordperfect 9
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/952,955C
 ; FILING DATE: 24-September-2001
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 09/938,275
 ; FILING DATE: 22-August-2001
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ;

NAME: Dwyer, Patrick M.
; REGISTRATION NUMBER: 32,411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 343-7074
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: Also referred to in the specification as 'AB 1-42'
US-09-952-95C-37

Query Match 100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGTVIA 42
Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGTVIA 42

RESULT 5
US-09-848-616-174
; Sequence 174, Application US/09848616
; Publication No. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Seehel, Peter
; APPLICANT: Durant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700_0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 174
LENGTH: 42
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amyloid Beta Peptide
US-09-848-616-174

Query Match 100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGTVIA 42
Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGTVIA 42

RESULT 6
US-09-865-294-65
; Sequence 65, Application US/09865294
; Publication No. US20030088325A1
; GENERAL INFORMATION:
; APPLICANT--Wang-Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0

Query Match 100.0%; Score 217; DB 10; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.5e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLYFFAEDVGSNKGAIIGLMYGGVVIA 42
 Db 1 DAEFRHDSGYEVHQKLYFFAEDVGSNKGAIIGLMYGGVVIA 42

RESULT 9
 US-09-731-460-1
 ; Sequence 1, Application US/09731460
 ; Patent No. US20020137112A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chojkier, Mario
 ; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
 ; TITLE OF INVENTION: Disease
 ; CURRENT APPLICATION NUMBER: US/09/731,460
 ; FILE REFERENCE: CHOJKIER-04302
 ; CURRENT FILING DATE: 2000-12-07
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 42
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; SEQ ID NO 731-460-1

Query Match 100.0%; Score 217; DB 10; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.5e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLYFFAEDVGSNKGAIIGLMYGGVVIA 42
 Db 1 DAEFRHDSGYEVHQKLYFFAEDVGSNKGAIIGLMYGGVVIA 42

RESULT 10
 US-10-076-708-7
 ; Sequence 7, Application US/10076708
 ; Patent No. US2002016657A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sharma, Satish
 ; APPLICANT: Rank, Kenneth
 ; TITLE OF INVENTION: Assays for Accessing Aa-Tau Aggregation
 ; FILE REFERENCE: 6322
 ; CURRENT APPLICATION NUMBER: US/10/076,708
 ; CURRENT FILING DATE: 2002-02-15
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 43
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; SEQ ID NO 10-076-708-7

Query Match 100.0%; Score 217; DB 9; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLYFFAEDVGSNKGAIIGLMYGGVVIA 42
 Db 1 DAEFRHDSGYEVHQKLYFFAEDVGSNKGAIIGLMYGGVVIA 42

RESULT 11
 US-10-051-496-1
 ; Sequence 1, Application US/10051496
 ; Publication No. US20020182660A1
 ; GENERAL INFORMATION:

RESULT 12
 US-10-217-459-1
 ; Sequence 1, Application US/10217459

APPLICANT: Kei-Lai L. Fong
 TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for
 Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-42) and Abeta (1-13)
 NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kei-Lai L. Fong
 STREET: 1004 West 8th Avenue
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.50 inch, 1.44MB storage
 COMPUTER: IBM PC Compatibles
 OPERATING SYSTEM: Windows
 SOFTWARE: MS No. US20020182660A1epad

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/051,496
 FILING DATE: 18-Jan-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/784,854A
 FILING DATE: 16-Feb-2001
 APPLICATION NUMBER: 60/183,407
 FILING DATE: 18-February-2000
 ATTORNEY/AGENT INFORMATION:
 NAME: Koenig, C. Frederick III
 REGISTRATION NUMBER: 29,662
 REFERENCE/DOCKET NUMBER: PBI-PTR001.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-6400
 TELEFAX: (215) 568-6499
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 43 Amino Acid
 TYPE: Amino Acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: <Unknown>
 ANTI-SENSE: <Unknown>
 ORIGINAL SOURCE:
 ORGANISM: <Unknown>
 INDIVIDUAL ISOLATE: <Unknown>
 CELL TYPE: <Unknown>
 IMMEDIATE SOURCE:
 LIBRARY: <Unknown>
 CLONE: <Unknown>
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 RELEVANT RESIDUES IN SEQ ID NO: 1 FROM 1 TO 43
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1;

US-10-051-496-1

Query Match 100.0%; Score 217; DB 9; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLYFFAEDVGSNKGAIIGLMYGGVVIA 42
 Db 1 DAEFRHDSGYEVHQKLYFFAEDVGSNKGAIIGLMYGGVVIA 42

RESULT 11
 US-10-051-496-1
 ; Sequence 1, Application US/10051496
 ; Publication No. US20020182660A1
 ; GENERAL INFORMATION:

Publication No. US20030069445A1
 GENERAL INFORMATION:
 APPLICANT: AUDIA, James
 APPLICANT: HYSLOP, Paul
 APPLICANT: NISSEN, Jeffrey
 APPLICANT: THOMPSON, Richard
 APPLICANT: TUNG, Jay
 APPLICANT: TANNER, Laura
 TITLE OF INVENTION: BIOLOGICAL REAGENTS AND METHODS FOR DETERMINING THE MECHANISM IN THE GENERATION OF BETA-AMYLOID PEPTIDE
 FILE REFERENCE: 002010-3544
 CURRENT APPLICATION NUMBER: US/10/217,459
 CURRENT FILING DATE: 2002-08-14
 PRIOR APPLICATION NUMBER: US 09/164,390
 PRIOR FILING DATE: 1998-09-30
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 1
 LENGTH: 43
 TYPE: PRT
 ORGANISM: beta-amyloid precursor protein
 US-10-217-459-1

RESULT 13
 US-09-28-966-1
 Query Match Score 100.0%; DB 9; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 42; Conservative 0; Mismatches 0;
 Gaps 0;
 Indels 0;
 Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42

NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis, LLP
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/280,966
 FILING DATE: 30-Mar-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/976,191
 FILING DATE: 21-Nov-1997
 APPLICATION NUMBER: 60/077,175
 FILING DATE: 22-Nov-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Swiss, Gerald F.
 REGISTRATION NUMBER: 30,113

TITLE OF INVENTION: ACID ESTERS, PHARMACEUTICAL COMPOSITIONS COMPRISING SAME, AND METHODS FOR INHIBITING -AMYLOID PEPTIDE RELEASE AND/OR ITS
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis, LLP
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/280,966
 FILING DATE: 30-Mar-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/976,191
 FILING DATE: 21-Nov-1997
 APPLICATION NUMBER: 60/077,175
 FILING DATE: 22-Nov-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Swiss, Gerald F.
 REGISTRATION NUMBER: 30,113

REFERENCE/DOCKET NUMBER: 002010-335
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-622-2300
 TELEFAX: 650-622-2499
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 43 amino acids
 TYPE: amino acid
 MOLECULE TYPE: peptide
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-280-966-1

Query Match Score 100.0%; DB 10; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 42; Conservative 0; Mismatches 0;
 Gaps 0;
 Indels 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 14
 US-09-904-987-1
 Sequence 1, Application US/09904987
 ; Patent No. US2003/908A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NO. US20020037908Abactyl, Inc.
 ; TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Preparative Assembly or Aggregation
 ; FILE REFERENCE: 42108/26146
 ; CURRENT APPLICATION NUMBER: US/09/904,987
 ; CURRENT FILING DATE: 2001-07-12
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 1
 ; LENGTH: 43
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: NCBI ENTREZ / QRHQA4
 ; DATABASE ENTRY DATE: 2000-09-15
 ; RELEVANT RESIDUES: (672)..(714)
 ; US-09-904-987-1

Query Match Score 100.0%; DB 10; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 42; Conservative 0; Mismatches 0;
 Gaps 0;
 Indels 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 15
 US-09-808-037-3
 Sequence 3, Application US/09808037
 ; Patent No. US20020052311A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SOLOMON, Beka
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF NEUROLOGICAL DISEASES AND DISORDERS
 ; FILE REFERENCE: SOLOMON-2D
 ; CURRENT APPLICATION NUMBER: US/09/808,037
 ; CURRENT FILING DATE: 2001-03-15
 ; PRIOR APPLICATION NUMBER: 09/629,971
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: US 09/473,653
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: US 60/152,417
 ; PRIOR FILING DATE: 1999-09-03
 ; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.0
; SEQ_ID NO 3
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-3

Query Match 100.0%; Score 217; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 1 6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLYFFAEDVGSNKGAIIGLMVGGVIA 42
Db 1 DAEFRHDSGYEVHHQKLYFFAEDVGSNKGAIIGLMVGGVIA 42

Search completed: April 21, 2003, 12:08:28
Job time : 15 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:39:48 ; Search time 11.5 Seconds
(without alignments),
25.585 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 ABFRHDSGY 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues
Word size : 0

Total number of hits satisfying chosen parameters: 68033

Minimum DB seq length: 5
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA.*

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5: /cgn2_6/podata/1/1aa/PCTRUS_COMB.pep:*
6: /cgn2_6/podata/1/1aa/backfiles1.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	9	90.0	10	1	US-08-371-930-12	Sequence 12, Appl
2	9	90.0	10	5	PCT-US94-01712-12	Sequence 36, Appl
3	5	50.0	5	4	US-08-617-267C-36	Sequence 8, Appl
4	4	40.0	6	1	US-07-843-949A-8	Sequence 3, Appl
5	4	40.0	6	2	US-08-218-978-B	Sequence 82, Appl
6	4	40.0	7	3	US-08-103-061-3	Patent No. 5117197
7	4	40.0	7	4	US-09-173-941-82	Sequence 1, Appl
8	4	40.0	9	6	5177197-3	Sequence 19, Appl
9	4	40.0	10	1	US-07-766-351-1	Sequence 119, Appl
10	4	40.0	10	1	US-08-059-032-1	Sequence 19, Appl
11	4	40.0	10	2	US-08-764-640-119	Sequence 63, Appl
12	4	40.0	10	2	US-08-559-084A-19	Sequence 64, Appl
13	4	40.0	10	3	US-08-973-225-119	Sequence 119, Appl
14	4	40.0	10	3	US-09-244-298A-119	Sequence 119, Appl
15	4	40.0	10	4	US-08-480-332-9	Sequence 19, Appl
16	4	40.0	10	4	US-08-660-531-19	Sequence 119, Appl
17	4	40.0	10	4	US-09-916-704-119	Sequence 63, Appl
18	4	40.0	10	4	US-09-548-372D-63	Sequence 64, Appl
19	4	40.0	10	4	US-09-548-372D-64	Sequence 63, Appl
20	4	40.0	10	4	US-09-548-367D-63	Sequence 64, Appl
21	4	40.0	10	4	US-09-548-367D-64	Sequence 1, Appl
22	4	40.0	10	5	PCT-US91-07290-1	Sequence 1, Appl
23	4	40.0	10	5	US-09-549-090-119	Sequence 5, Appl
24	3	30.0	5	1	US-07-750-330-1	Sequence 5, Appl
25	3	30.0	5	1	US-07-750-330-2	Sequence 5, Appl
26	3	30.0	5	1	US-07-750-330-5	Sequence 5, Appl
27	3	30.0	5	1	US-07-780-790A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-371-930-12
; Sequence 12, Application US/08371930
; Patent No. 5578451
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-371-930-12

Query Match Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRHDSGY 9
Db 2 AEFRHDSGY 10

RESULT 2
PCT-US94-01712-12
Sequence 12, Application PC/TUS9401712
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuo
TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01712
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US94 01712-12

Query Match 90.0%; Score 9; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRHDSGY 9
Db 2 AEFRHDSGY 10

RESULT 3
US-08-617-267C-36
Sequence 36, Application US/08617267C
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LATIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal
US-08-617-267C-36

Query Match 50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 HDSGY 9
Db 1 HDSGY 5

RESULT 4
US-07-843-949A-8
Sequence 8, Application US/0784394A
Patient No. 5340935
GENERAL INFORMATION:
APPLICANT: Anderson, Paul J.
APPLICANT: Streuli, Michel
APPLICANT: Schlossman, Stuart F.
TITLE OF INVENTION: DNAs Encoding Proteins Active In Lymphocyte-Mediated Cytotoxicity
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/843.949A
FILING DATE: 19920129
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/460,678
FILING DATE: January 5, 1990
APPLICATION NUMBER: 07/726,607
FILING DATE: July 10, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/021003

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 US-07-843-949A-8

Query Match Score 4; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 7 SGYE 10
 Db 1 SGYE 4

RESULT 6
 US-08-303-861-3
 Sequence 3, Application US/08303861
 Patent No. 6086902
 GENERAL INFORMATION:
 APPLICANT: ZAMB, TIMOTHY
 APPLICANT: LIANG, XIAOPTING
 APPLICANT: PABLUX, LORNE A.
 TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/303,861
 FILING DATE: 09-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARK, FREDDIE K.
 REGISTRATION NUMBER: 35,636
 REFERENCE/DOCKET NUMBER: 20310-20020-20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-303-861-3

Query Match Score 4; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 6 DSGY 9
 Db 2 DSGY 5

RESULT 7
 US-09-173-941-82
 Sequence 82, Application US/09173941
 Patent No. 6140081
 GENERAL INFORMATION:
 APPLICANT: BARBAS, Carlos F.
 TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
 FILE REFERENCE: NOV0081S
 CURRENT APPLICATION NUMBER: US/09/173,941
 CURRENT FILING DATE: 1998-10-16
 NUMBER OF SEQ ID NOS: 120
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 82
 LENGTH: 7

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 US-08-218-978-8

Query Match Score 4; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+05;

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; TYPE: PRT ; REFERENCE/DOCKET NUMBER: 17796-002
; ORGANISM: Artificial Sequence ; TELECOMMUNICATION INFORMATION:
; FEATURE: ; TELEPHONE: (415) 877-0900
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide ; TELEFAX: (415) 877-8370
; US-09-173-941-82 ; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; Molecule Type: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= "Xaa4 can be either Glu or Lys"
; OTHER INFORMATION: /note= "Xaa4 can be either Glu or Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= "Xaa5 can be either Met or Nle"
; OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
US-07-766-351-1
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Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
Qy 4 RHDS 7
Db 1 RHDS 4

Query Match Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
Qy 6 DSGY 9
Db 5 DSGY 8

Query Match Score 4; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-08-059-032-1
Sequence 1, Application US/08059032
; Patent No. 5424205
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seubert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnstone, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Stewart Street Tower,
; SUITE: Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/059,032
; FILING DATE: 1993/05/07
; CLASSIFICATION: A35
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William E.
; REGISTRATION NUMBER: 30-223
; REFERENCE/DOCKET NUMBER: 15270-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; Molecule Type: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= "Xaa4 can be either Glu or Lys"
; OTHER INFORMATION: /note= "Xaa4 can be either Glu or Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= "Xaa5 can be either Met or Nle"
; OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
US-07-766-351-1
Query Match Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 65; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFR 4
Db 7 AEFR 10

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LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /label= Xaa4
 /note= "Xaa4 can be either Gln or Lys"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 5
 OTHER INFORMATION: /label= Xaa5
 /note= "Xaa5 can be either Met or Nle"
 US-08-059-032-1
 Query Match 40.0%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFR 4
 Db 111
 Db 4 AEFR 7

RESULT 12
 US-08-659-984A-19
 Sequence 19 Application US/08659984A
 Patent No. 5942400
 GENERAL INFORMATION:
 APPLICANT: Anderson, John P.
 APPLICANT: Sinha, Sukanto
 APPLICANT: Jacobson-Croak, Kirsten L.
 TITLE OF INVENTION: Assays for Detecting Beta-Secretase
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Ctr., 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/659,984A
 FILING DATE: 07-JUN-1996
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/485,152
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Heslin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15270-002810US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Region
 LOCATION: one-of(1)
 OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
 US-08-659-984A-19
 Query Match 40.0%; Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFR 4
 Db 111
 Db 7 AEFR 10

LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 NAME/KEY: Hrubec, Robert T.
 LOCATION: 36, 392
 REGISTRATION NUMBER: PK3281
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 119:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids

RESULT 13
US-08-973-225-119
; Sequence 119, Application US/08973225A
; Patent No. 6083913
GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,225A
; FILING DATE: 04-DEC-1997
; ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 119:
US-08-973-225-119

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 AEFR 4
Db 4 AEFR 7

RESULT 14
US-09-244-298A-119
; Sequence 119, Application US/09244298A
; Patent No. 612238
GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Gates, Christian
; Schatz, Peter J.
; Balasubramanian, Palaniappan
; Wagstrom, Christopher R.
; Hendren, Richard W.
; Deprince, Randolph B.

Query Match 40.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 AEFR 4
Db 4 AEFR 7

RESULT 15
US-09-244-298A-119
; Sequence 9, Application US/09244298A
; Patent No. 6180134
GENERAL INFORMATION:
; APPLICANT: Zalipsky, Samuel; Woodle, Martin; Martin, Francis;
; Barenholz, Yechiel
; TITLE OF INVENTION: Enhanced Circulation Effector Composition and
; Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; ZIP: 94306
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,332
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/316,436

; FILING DATE: 29-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/035,443
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOLINI, JUDY M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5325-0115.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Peptide 9, Fig. 13
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; US-08-430-332-9

Query Match Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

QY	6	DSGY	9
Db	3	DSGY	6

Search completed: April 21, 2003, 12:43:00
Job time : 11.5 secs



GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:40:48 ; search time 11.5 Seconds
(without alignments)
65.751 Million cell updates/sec

Title: US-09-580-018-10
Perfect score: 10
Sequence: 1 AEFRHDSGYE 10

Scoring table: OLIGO
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Searched: 288829 seqs, 75613885 residues

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 * Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	90.0	10	9 US-09-865-294-69	Sequence 69, Appli
2	6	60.0	7	10 US-09-867-847-5	Sequence 5, Appli
3	5	50.0	5	10 US-09-872-445-36	Sequence 36, Appli
4	4	40.0	5	10 US-09-874-927-72	Sequence 72, Appli
5	4	40.0	5	10 US-09-875-847-72	Sequence 72, Appli
6	4	40.0	5	10 US-09-879-748-72	Sequence 72, Appli
7	4	40.0	5	10 US-09-879-927-63	Sequence 72, Appli
8	4	40.0	5	10 US-09-879-927-63	Sequence 72, Appli
9	4	40.0	5	10 US-09-881-442-72	Sequence 72, Appli
10	4	40.0	6	10 US-09-880-037-7	Sequence 7, Appli
11	4	40.0	8	10 US-09-884-718-10	Sequence 10, Appli
12	4	40.0	10	9 US-09-895-903A-4	Sequence 4, Appli
13	4	40.0	10	9 US-09-895-903A-5	Sequence 5, Appli
14	4	40.0	10	10 US-09-894-927-63	Sequence 63, Appli
15	4	40.0	10	10 US-09-894-927-64	Sequence 64, Appli
16	4	40.0	10	10 US-09-895-847-63	Sequence 63, Appli
17	4	40.0	10	10 US-09-895-947-64	Sequence 63, Appli
18	4	40.0	10	10 US-09-894-943-63	Sequence 63, Appli
19	4	40.0	10	10 US-09-894-743-64	Sequence 64, Appli

ALIGNMENTS

RESULT 1
US-09-865-294-69
; Sequence 69, Application US/09865294
; Publication No. US20030068325A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic Peptide composition as vaccines for the prevention and treatment of Alzheimer's Disease
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: US/09/865,294
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 69
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-294-69

Query Match
Best Local Similarity 90.0%; Score 9; DB 9; Length 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-867-847-5
; Sequence 5, Application US/09867847
; Patent No. US2003009435A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASES
; FILE REFERENCE: 1444-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
 ; PRIOR FILING DATE: 1999-11-39
 ; PRIOR APPLICATION NUMBER: 09/724,842
 ; PRIOR FILING DATE: 2000-11-28
 ; OTHER INFORMATION: SEQ ID NOS: 65
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 5
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
 ; OTHER INFORMATION: or Peptidomimetics
 ; US-09-867-847-5

Query Match 60.0%; Score 6; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy	1 AEFRHD 6	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	2 AEFRHD 7	Qy 5 HDSGY 9 Db 1 HDSGY 5

RESULT 4

US-09-794-927-72
 ; Sequence 72, Application US/09794927
 ; Patent No. US010101624A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Biernowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang A.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 ; TITLE OF INVENTION: USES
 ; FILE REFERENCE: 28341/6280FG
 ; CURRENT APPLICATION NUMBER: US/09/794,927
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIORITY NUMBER: 09/416,501
 ; PRIORITY FILING DATE: 1999-10-13
 ; PRIORITY APPLICATION NUMBER: 60/155,493
 ; PRIORITY FILING DATE: 1999-09-23
 ; PRIORITY APPLICATION NUMBER: 09/404,133
 ; PRIORITY FILING DATE: 1999-09-23
 ; PRIORITY APPLICATION NUMBER: PC1/US99/20881
 ; PRIORITY FILING DATE: 1999-09-23
 ; PRIORITY APPLICATION NUMBER: 60/101,594
 ; PRIORITY FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SEQ ID NO: 72
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-09-794-927-72

Query Match 40.0%; Score 4; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AEFR 4	Qy 1 AEFR 4
Db	2 AEFR 5	Db 2 AEFR 5

RESULT 5

US-09-795-847-72
 ; Sequence 72, Application US/09795847
 ; Patent No. US2001018208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Biernowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang A.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 ; TITLE OF INVENTION: USES
 ; FILE REFERENCE: 28341/6280DE
 ; CURRENT APPLICATION NUMBER: US/09/795,847
 ; CURRENT FILING DATE: 2001-02-28
 ; PRIORITY NUMBER: 09/416,901
 ; PRIORITY FILING DATE: 1999-10-13
 ; PRIORITY APPLICATION NUMBER: 60/155,493
 ; PRIORITY FILING DATE: 1999-09-23
 ; PRIORITY APPLICATION NUMBER: 09/404,133
 ; PRIORITY FILING DATE: 1998-09-24

Query Match 50.0%; Score 5; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;

PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-795-847-72

Query Match	40.0%	Score 4;	DB 10;	Length 5;	
Best Local Similarity	10.0%	Pred. No.	2.6e+05;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1 AEFR 4				
Db	1111				
	2 AEFR 5				

RESULT 6
US-09-794-743-72
; Sequence 72, Application US/09794743
; Patent No. US2001021391A1

GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-794-748-72

Query Match	40.0%;	Score 4;	DB 10;	Length 5;	
Best Local Similarity	10.0%;	Pred. No.	2.6e+05;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1 AEFR 4				
Db	1111				
	2 AEFR 5				

RESULT 8
US-09-794-925-72
; Sequence 72, Application US/09794925
; Patent No. US20020064819A1

GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-794-743-72

Query Match	40.0%;	Score 4;	DB 10;	Length 5;	
Best Local Similarity	10.0%;	Pred. No.	2.6e+05;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1 AEFR 4				
Db	1111				
	2 AEFR 5				

RESULT 7
US-09-794-748-72
; Sequence 72, Application US/09794748
; Patent No. US20020037315A1

OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFR 4
1111
Db 2 AEFR 5

RESULT 9
US-09-681-442-72
; Sequence 72, Application US/09681442
; Patent No. US20020081634A1

GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 28341/6280RG

CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIORITY NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIORITY NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: FCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; PRIORITY NUMBER: 09/309,73
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-72

Query Match 40.0%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFR 4
1111
Db 2 AEFR 5

RESULT 10
US-09-808-037-7
; Sequence 7, Application US/09808037
; Patent No. US20020052311A1

GENERAL INFORMATION:
; APPLICANT: SOLONIN, Beka
; APPLICANT: HANAN, Bilal
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON-2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; PRIOR APPLICATION NUMBER: 2000-07-31
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417

Query Match 40.0%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFR 4
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Db      2 AEFR 5
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-795-903A-5

RESULT 12
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; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; FEATURE: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4

Query Match      40.0%; Score 4; DB 9; Length 10;
-Best Local Similarity 100.0%; Pred. No. 89;
-Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy    1 AEFR 4
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Db    7 AEFR 10

RESULT 13
;
; Sequence 5, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; FEATURE: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794 927-63

Query Match      40.0%; Score 4; DB 10; Length 10;
-Best Local Similarity 100.0%; Pred. No. 89;
-Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy    1 AEFR 4
      1 1 1
Db    7 AEFR 10

RESULT 14
;
; Sequence 63, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28441/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794 927-63

Query Match      40.0%; Score 4; DB 10; Length 10;
-Best Local Similarity 100.0%; Pred. No. 89;
-Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy    1 AEFR 4
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Db    7 AEFR 10

RESULT 15
;
; Sequence 64, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; 
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; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; PRIORITY NUMBER: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: US-09-794-927-64

Query Match          40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AEFR 4
          |||
Db      7 AEFR 10
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Search completed: April 21, 2003, 12:43:30
Job time : 12 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:08:35 ; Search time 10 Seconds
(without alignments)
29.423 Million cell updates/sec

Title: US-09-580-018-8
Perfect score: 10
Sequence: 1 MDAFRHDSG 10

Scoring table: OLIGO
Gapext 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0
Maximum DB seq length: 10

Post processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	9	90.0	10	1	US-08-371-930-12	Sequence 12, Appl
2	9	90.0	10	5	PCT-US94-01712-12	Sequence 12, Appl
3	6	60.0	10	4	US-08-548-372D-64	Sequence 64, Appl
4	6	60.0	10	4	US-09-548-367D-64	Sequence 64, Appl
5	5	50.0	5	2	US-08-422-333-7	Sequence 7, Appl
6	5	50.0	5	6	5187153-6	Patent No. 5187153
7	5	50.0	5	6	5220013-6	Patent No. 5220013
8	5	50.0	5	6	5223482-6	Patent No. 5223482
9	5	50.0	7	2	US-08-792-553-10	Sequence 10, Appl
10	5	50.0	8	4	US-09-548-372D-67	Sequence 67, Appl
11	5	50.0	8	4	US-08-548-367D-67	Sequence 67, Appl
12	5	50.0	9	3	US-08-802-981-221	Sequence 221, Appl
13	5	50.0	9	4	US-09-294-987-6	Sequence 6, Appl
14	5	50.0	10	1	US-08-766-351-1	Sequence 1, Appl
15	5	50.0	10	1	US-08-059-032-1	Sequence 1, Appl
16	5	50.0	10	2	US-08-025-321C-1	Sequence 1, Appl
17	5	50.0	10	2	US-08-659-984A-19	Sequence 19, Appl
18	5	50.0	10	4	US-08-660-531-19	Sequence 19, Appl
19	5	50.0	10	4	US-09-548-372D-63	Sequence 63, Appl
20	5	50.0	10	4	US-08-548-367D-63	Sequence 63, Appl
21	4	40.0	4	5	PCT-US91-07290-1	Sequence 1, Appl
22	4	40.0	4	4	US-09-513-783A-92	Sequence 92, Appl
23	4	40.0	5	4	US-08-617-267C-36	Sequence 36, Appl
24	4	40.0	7	1	US-08-136-743B-33	Sequence 33, Appl
25	4	40.0	7	1	US-08-136-743B-35	Sequence 35, Appl
26	4	40.0	7	1	US-08-136-743B-56	Sequence 56, Appl
27	4	40.0	7	3	US-09-040-216-29	Sequence 29, Appl

Sequence 82, Appl
Sequence 219, Appl
Sequence 220, Appl
Sequence 119, Appl
Sequence 119, Appl
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Sequence 119, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 9, Appl
Sequence 5, Appl
Sequence 2, Appl
Sequence 33, Appl
Sequence 1, Appl
Sequence 114, Appl
Sequence 115, Appl
Sequence 169, Appl

ALIGNMENTS

RESULT 1
US-08-371-930-12
; Sequence 12, Application US/08371-930
; Patent No. 5578451
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,930
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-371-930-12
Query Match 90.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Qy 2 DAEFRHDSG 10
Db 1 DAEFRHDSG 9

RESULT 2

; Sequence 12, Application PC/TUS9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-0804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01712
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/019,208
FILING DATE: February 18, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/154001
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

PCT/US94-01712-12

Query Match 90.0%; Score 9; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 9; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 2 DAEFRHDSG 10
Db 1 DAEFRHDSG 9

RESULT 3

; Sequence 64, Application US/09548372D
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-548-372D-64

Query Match 60.0%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 MDAEFR 6
Db 5 MDAEFR 10

RESULT 4

; Sequence 64, Application US/09548367D
; Patent No. 644698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-548-367D-64

Query Match 60.0%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 MDAEFR 6
Db 5 MDAEFR 10

RESULT 5

; Sequence 7, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; ADDRESSSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0., Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/422,333
 FILING DATE: 13-APR-1995
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Shearer, Peter R.
 REGISTRATION NUMBER: 28,117
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 966-1550
 TELEFAX: (415) 968-2438
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 S-08-422-333-7

Query Match 50.0%; Score 5; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MDAEF 5
 1|||
 1 MDAEF 5

RESULT 6
 Patent No. 5187153
 APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
 TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
 AMYLOID POLYPEPTIDE DERIVATIVES
 NUMBER OF SEQUENCES: 33
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/502,273
 FILING DATE: 29-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 361,912
 FILING DATE: 06-JUN-1989
 APPLICATION NUMBER: 359,911
 FILING DATE: 12-MAY-1989
 APPLICATION NUMBER: 87,002
 FILING DATE: 18-AUG-1987
 APPLICATION NUMBER: 8,810
 FILING DATE: 30-JAN-1987
 APPLICATION NUMBER: 948,376
 FILING DATE: 31-DEC-1986
 APPLICATION NUMBER: 948,376
 FILING DATE: 30-JAN-1987
 APPLICATION NUMBER: 8,810
 FILING DATE: 17-NOV-1986
 SEQ ID NO:6;
 LENGTH: 5

Query Match 50.0%; Score 5; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MDAEF 5
 1|||
 1 MDAEF 5

RESULT 7
 Patent No. 5220013-6
 APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
 TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
 OF ALZHEIMER'S DISEASE
 NUMBER OF SEQUENCES: 30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/444,118
 FILING DATE: 30-NOV-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 87,002
 FILING DATE: 18-AUG-1987
 APPLICATION NUMBER: 8,810
 FILING DATE: 30-JAN-1987
 APPLICATION NUMBER: 948,376
 FILING DATE: 31-DEC-1986
 APPLICATION NUMBER: 932,193
 FILING DATE: 17-NOV-1986
 SEQ ID NO:6;
 LENGTH: 5

Query Match 50.0%; Score 5; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MDAEF 5
 1|||
 1 MDAEF 5

RESULT 8
 Patent No. 5223482-6
 APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL,
 BARBARA
 TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
 INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
 NUMBER OF SEQUENCES: 34
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/361,912
 FILING DATE: 06-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 359,911
 FILING DATE: 12-MAY-1989
 APPLICATION NUMBER: 87,002
 FILING DATE: 18-AUG-1987
 APPLICATION NUMBER: 8,810
 FILING DATE: 30-JAN-1987
 APPLICATION NUMBER: 948,376
 FILING DATE: 31-DEC-1986
 APPLICATION NUMBER: 932,193
 FILING DATE: 17-NOV-1986
 SEQ ID NO:6;
 LENGTH: 5

Query Match 50.0%; Score 5; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;

1 MDAEF 5
 1|||
 1 MDAEF 5

RESULT 9
 US-08-792-553-10
 Sequence 10, Application US/08792553
 Patent No. 5981200
 GENERAL INFORMATION:
 APPLICANT: Tsien, Roger Y.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Heim, Roger
 TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 FISH & RICHARDSON P.C.
 ADDRESSEES:

STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: California
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/792,553
 FILING DATE: 31-JAN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lisa A. Halle, Ph.D.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07257/041001/UC 96-160-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-678-5070
 TELEXFAX: 619-678-5099
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-792-553-10

Query Match 50.0%; Score 5; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5
 Db 3 MDAEF 7

RESULT 10

US-09-548-372D-67

Sequence 67, Application US/09548372D

GENERAL INFORMATION:

APPLICANT: GURNEY ET AL.
 TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 29915/6280J
 ; CURRENT APPLICATION NUMBER: US/09/548,372D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; NUMBER OF SEQ ID NOS: 73
 ; SEQ ID NO 67
 ; SOFTWARE: PatentIn version 3.1
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptide

Query Match 50.0%; Score 5; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5

Db 4 MDAEF 8
 RESULT 11

US-09-548-367D-67

Sequence 67, Application US/09548367D

GENERAL INFORMATION:

APPLICANT: GURNEY ET AL.
 TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 29915/6280J
 ; CURRENT APPLICATION NUMBER: US/09/548,367D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; NUMBER OF SEQ ID NOS: 73
 ; SEQ ID NO 67
 ; SOFTWARE: PatentIn version 3.1
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptide

Query Match 50.0%; Score 5; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEF 5

Db 4 MDAEF 8
 RESULT 12

US-08-002-981-221

Sequence 221, Application US/08802981

GENERAL INFORMATION:

APPLICANT: Komoriya, Akira
 ; TITLE OF INVENTION: Compositions for the Detection of Enzyme
 ; COMPOSITIONS AND METHODS OF USE THEREOF
 ; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
 ; NUMBER OF SEQUENCES: 231
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/802,981
 ; FILING DATE: 20-FEB-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunter, Tom
 ; REGISTRATION NUMBER: 38,498
 ; REFERENCE/DOCKET NUMBER: 016865-000300US
 ; TELECOMMUNICATION INFORMATION:

Page 5

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; NAME: Smith, William E.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15270-10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 4  
; OTHER INFORMATION: /label= "Xaa4  
; OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"  
FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 5  
; OTHER INFORMATION: /label= "Xaa5  
; OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"  
US-08-059-032-1
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Query Match 50.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 DAEFR 6  
Db 6 DAEFR 10
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Search completed: April 21, 2003, 12:12:56
Job time : 11 secs

; PRIOR APPLICATION NUMBER: 60/168,594
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/724,842
 ; PRIOR FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 5
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
 ; OTHER INFORMATION: or peptidomimetics
 US-09-867-847-5

Qy	2	DAEFRHD	8
Db	1	DAEFRHD	7

Query Match 70.0%; Score 7; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
 ; FILE REFERENCE: OMRF 179
 ; CURRENT APPLICATION NUMBER: US/09/795,903A
 ; CURRENT FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 09/604,608
 ; PRIOR FILING DATE: 2000-06-17
 ; PRIOR APPLICATION NUMBER: 60/168,060
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: 60/177,836
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 60/178,368
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: 60/210,292
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 4
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-795-903A-4

RESULT 3

Qy	1	MDAEFR	6
Db	5	MDAEFR	10

Query Match 60.0%; Score 6; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 ; TITLE OF INVENTION: USES
 ; FILE REFERENCE: 28341/6280FG
 ; CURRENT APPLICATION NUMBER: US/09/794,927
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 64
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-795-847-64

RESULT 5

Qy	1	MDAEFR	6
Db	5	MDAEFR	10

Query Match 60.0%; Score 6; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TITLE OF INVENTION: USES
 ; FILE REFERENCE: 28341/6280DE
 ; CURRENT APPLICATION NUMBER: US/09/795,847
 ; PRIOR APPLICATION NUMBER: US2001018208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Bienkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 ; TITLE OF INVENTION: USES
 ; FILE REFERENCE: 28341/6280DE
 ; CURRENT APPLICATION NUMBER: US/09/795,847
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 64
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-795-847-64

RESULT 4

Qy	1	MDAEFR	6
Db	5	MDAEFR	10

Query Match 60.0%; Score 6; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36e+00;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 ; TITLE OF INVENTION: USES
 ; FILE REFERENCE: 28341/6280FG
 ; CURRENT APPLICATION NUMBER: US/09/794,927
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 64
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-795-847-64

Query Match 60.0%; Score 6; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
 Db 5 MDAEFR 10

RESULT 6
 US-09-794-743-64
 ; Sequence 64, Application US/09794743
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Blenkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 283416280BC
 ; CURRENT APPLICATION NUMBER: US/09/794,743
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 64
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0

RESULT 7
 US-09-794-748-64
 ; Sequence 64, Application US/09794748
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Blenkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 283416280JL
 ; CURRENT APPLICATION NUMBER: US/09/794,748
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13

Query Match 60.0%; Score 6; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAEFR 6
 Db 5 MDAEFR 10

RESULT 8
 US-09-796-264-4
 ; Sequence 4, Application US/09796264
 ; Patent No. US20049303A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Jordan J. N.
 ; APPLICANT: Lin, Xinli
 ; APPLICANT: Koelsch, Gerald
 ; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
 ; TITLE OF INVENTION: Of Use Thereof
 ; FILE REFERENCE: OMRF 179
 ; CURRENT APPLICATION NUMBER: US/09/796,264
 ; CURRENT FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 09/604,608
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: 60/168,060
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: 60/177,836
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 60/178,368
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: 60/210,292
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 31
 ; SEQ ID NO 4
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.1

RESULT 9
 US-09-794-925-64
 ; Sequence 64, Application US/09794925
 ; Patent No. US2004819A1
 ; Sequence 64, Application US/09794925
 ; Patent No. US2004819A1

; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 2834.1/6280FG
; CURRENT APPLICATION NUMBER: US/09/794, 925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416, 301
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155, 493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404, 133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101, 594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-794 925-64

Query Match 60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0..36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEFR 6
Db 5 MDAEFR 10

RESULT 10
US-09-681-442-64
; Sequence 64, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 2834.1/6280FG
; CURRENT APPLICATION NUMBER: US/09/681, 442
; PRIOR APPLICATION NUMBER: 09/416, 301
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155, 493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404, 133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-681-442-64

Query Match 60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0..36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEFR 6
Db 5 MDAEFR 10

RESULT 11
US-09-845-226-4
; Sequence 4, Application US/09845226
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845, 226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603, 713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,.060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177, 836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178, 368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210, 292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-845-226-4

Query Match 60.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0..36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDAEFR 6
Db 5 MDAEFR 10

RESULT 12
US-09-794-927-72
; Sequence 72, Application US/09794927
; Patent No. US2001016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 2834.1/6280FG
; CURRENT APPLICATION NUMBER: US/09/794, 927
; PRIOR APPLICATION NUMBER: 09/416, 901
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416, 301
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404, 133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US20010018208A1
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-72

Qy 2 DAEFR 6
  1||| 1 DAEFR 5
Db 1 DAEFR 6
  1||| 1 DAEFR 5

RESULT 13
US-09-795-847-72
Sequence 72, Application US/09795847
; Patent No. US20010018208A1
GENERAL INFORMATION:
; GENERAL INFORMATION: Gurney, Mark E.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US/09/795,847
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-72

Qy 2 DAEFR 6
  1||| 1 DAEFR 5
Db 1 DAEFR 6
  1||| 1 DAEFR 5

RESULT 14
US-09-794-748-72
Sequence 72, Application US/09794748
; Patent No. US20020037315A1
GENERAL INFORMATION:
; GENERAL INFORMATION: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US/09/794,748
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-72

Qy 2 DAEFR 6
  1||| 1 DAEFR 5
Db 1 DAEFR 6
  1||| 1 DAEFR 5

RESULT 14
US-09-794-743-72
Sequence 72, Application US/09794743
; Patent No. US20010021391A1

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-72
Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DAEFR 6
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Db 1 DAEFR 5

Search completed: April 21, 2003, 12:13:35
Job time : 11.3333 secs

GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model
 Run on: April 21, 2003, 12:08:35 ; Search time 10 seconds
 (without alignments)
 29,423 Million cell updates/sec

Title: US-09-580-018-9
 Perfect score: 10
 Sequence: DAEFRHDSGY 10

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:
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 2: /cgn2_6/ptodata/1/iaa/5B_COMBO.pep:
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 6: /cgn2_6/ptodata/1/iaa/backfiles_pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	10	100	0	10	1	US-09-371-930-12	Sequence 12, Appl
2	10	100	0	10	5	PCT-US9401712-12	Sequence 12, Appl
3	5	50	0	5	4	US-08-267C-36	Sequence 36, Appl
4	5	50	0	10	1	US-07-766-351-1	Sequence 1, Appl
5	5	50	0	10	1	US-08-059-032-1	Sequence 1, Appl
6	5	50	0	10	2	US-08-659-084A-19	Sequence 19, Appl
7	5	50	0	10	4	US-08-660-531-19	Sequence 19, Appl
8	5	50	0	10	4	US-09-548-372D-63	Sequence 63, Appl
9	5	50	0	10	4	US-09-548-372D-64	Sequence 64, Appl
10	5	50	0	10	4	US-09-548-367D-63	Sequence 63, Appl
11	5	50	0	10	4	US-09-548-367D-64	Sequence 64, Appl
12	5	50	0	10	5	PCT-US1-07290-1	Sequence 1, Appl
13	4	40	0	4	4	US-09-513-783A-92	Sequence 92, Appl
14	4	40	0	5	2	US-08-422-333-7	Sequence 7, Appl
15	4	40	0	5	6	5187153-6	Patent No. 5187153
16	4	40	0	5	6	5220013-6	Patent No. 5220013
17	4	40	0	6	5223432-6	Patent No. 5223432	
18	4	40	0	7	1	US-08-136-743B-33	Sequence 33, Appl
19	4	40	0	7	1	US-08-136-743B-35	Sequence 35, Appl
20	4	40	0	7	1	US-08-136-743B-56	Sequence 56, Appl
21	4	40	0	7	2	US-08-792-553-10	Sequence 10, Appl
22	4	40	0	7	3	US-09-040-216-29	Sequence 29, Appl
23	4	40	0	7	3	US-08-303-861-3	Sequence 3, Appl
24	4	40	0	7	4	US-09-173-941-02	Sequence 82, Appl
25	4	40	0	8	4	US-09-548-372D-67	Sequence 67, Appl
26	4	40	0	8	4	US-09-548-367D-67	Sequence 67, Appl
27	40.0	40.0	9	3	US-08-802-981-219	Sequence 219, Appl	

ALIGNMENTS

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RESULT 1
US-08-371-930-12
; Sequence 12, Application US/08371930
; Patent No. 5578451
; GENERAL INFORMATION:
;   APPLICANT: Nishimoto, Ikuo
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
;   NUMBER OF SEQUENCES: 30
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: U.S.A.
;     ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/371,930
;   FILING DATE:
;   CLASSIFICATION: 436
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/019,208
;     FILING DATE: February 18, 1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Clark, Paul T.
;     REGISTRATION NUMBER: 30,162
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (617) 542-5070
;       TELEFAX: (617) 542-8906
;       TELEX: 200154
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 10
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
US-08-371-930-12
Query Match Score 100.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e-0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGY 10
Db 1 DAEFRHDSGY 10

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RESULT 2 PCT-US94-01712-12

; Sequence 12, Application PC/TU9401712

; GENERAL INFORMATION:

; APPLICANT: Nishimoto, Ikuo

; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 502 or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.1)

; SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01712

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/019,208

FILING DATE: February 18, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/154001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-0700

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 10

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US94-01712-12

Query Match 100.0% Score 10; DB 5; Length 10;

Best Local Similarity 100.0% Pred. No. 1.1e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDGSY 10

Db 1 DAEFRHDGSY 10

RESULT 3 US-08-617-267C-36

; Sequence 36, Application US/08617267C

; Patent No. 6319498

GENERAL INFORMATION:

APPLICANT: Findley, Mark A. et al.

TITLE OF INVENTION: Modulators of Amyloid Aggregation

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/766351

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Lisabeth Feix

REGISTRATION NUMBER: 31547

REFERENCE/DOCKET NUMBER: 17796-002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 877-0900

TELEFAX: (415) 877-8370

RESULT 4 US-08-617-267C-36

; Sequence 1, Application US/07766351.

; Patent No. 5293652

GENERAL INFORMATION:

APPLICANT: Sinha, Sukanto

APPLICANT: Seubert, Peter A.

APPLICANT: Dovey, Harry F.

APPLICANT: McConlogue, Lisa C.

APPLICANT: Little, Sheila P.

APPLICANT: Johnstone, Edward M.

TITLE OF INVENTION: Amyloidin Protease and Uses Thereof

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Athena Neurosciences, Inc.

STREET: 800F Gateway Blvd.

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/766351

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Lisabeth Feix

REGISTRATION NUMBER: 31547

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

FEATURE: Modified-site

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /label= Xaa⁴

NOTE: "Xaa⁴ can be either Gln or Lys"

FEATURE: Modified-site

NAME/KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: /label= Xaa⁵

NOTE: "Xaa⁵ can be either Met or Nle"

US-07-766-351-1

Query Match 50.0%; Score 5; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 6 DAEFR 10

RESULT 5

US-08-059-032-1

Sequence 1, Application US/08059032

PATENT NO. 542405

GENERAL INFORMATION:

APPLICANT: Sinha, Sukanto

APPLICANT: Seubert, Peter A.

APPLICANT: Dovey, Harry F.

APPLICANT: McConlogue, Lisa C.

APPLICANT: Little, Sheila P.

APPLICANT: Johnstone, Edward M.

TITLE OF INVENTION: Amyloidin Protease and Uses Thereof

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Steuart Street Tower,

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/059_032

FILING DATE: 19930507

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William E.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15270-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

FEATURE: Modified-site

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /label= Xaa⁴

NOTE: "Xaa⁴ can be either Gln or Lys"

FEATURE: Modified-site

NAME/KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: /label= Xaa⁵

NOTE: "Xaa⁵ can be either Met or Nle"

US-08-059-032-1

Query Match 50.0%; Score 5; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 6 DAEFR 10

RESULT 6

US-08-659-984A-19

Sequence 19, Application US/08659984A

PATENT NO. 542400

GENERAL INFORMATION:

APPLICANT: Anderson, John P.

APPLICANT: Sinha, Sukanto

APPLICANT: Jacobson-Croak, Kirsten L.

TITLE OF INVENTION: Assays for Detecting Beta-Secretase

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/659, 984A

FILING DATE: 07-JUN-1996

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485, 152

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.

REGISTRATION NUMBER: 29, 541

REFERENCE/DOCKET NUMBER: 15270-002810US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: one-of-1)

NOTE: "N-terminal Ser is acetylated."

US-08-659-984A-19

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; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-372D-63

Query Match Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-08-660-531-19
; Sequence 19, Application US/08660531
; Patent No. 6221655
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Slnha, Sukanto
; APPLICANT: Kellm, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.N.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-0-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-526-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(1)
; OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
; OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
US-08-660-531-19

Query Match Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-09-548-372D-63
; Sequence 63, Application US/09548372D
; Patent No. 6420534

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US-09-548-367D-63
; Sequence 63, Application US/09548367D
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT FILING DATE: 2000-04-12
; PRIORITY NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide

US-09-548-367D-63
Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 6 DAEFR 10

RESULT 11
PCT-US91-07290-1
; Sequence 1, Application PC/TUS9107290
; GENERAL INFORMATION:
; APPLICANT: Sinha, Sukanto
; APPLICANT: Seibert, Peter A.
; APPLICANT: Dovey, Harry F.
; APPLICANT: McConlogue, Lisa C.
; APPLICANT: Little, Sheila P.
; APPLICANT: Johnston, Edward M.
; TITLE OF INVENTION: Amyloidin Protease and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Athena Neurosciences, Inc.
; STREET: 800F Gateway Blvd.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07290
; FILING DATE: 1991/004
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Lisabeth Feix
; REGISTRATION NUMBER: 31547
; REFERENCE/DOCKET NUMBER: 17796-002
; TELEPHONE: (415) 877-8370
; TELEFAX: (415) 877-8390
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Xaa4
; OTHER INFORMATION: /note= "Xaa4 can be either Gln or Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Xaa5
; OTHER INFORMATION: /note= "Xaa5 can be either Met or Nle"
; PCT-US91-07290-1
Query Match 50.0%; Score 5; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 6 DAEFR 10

RESULT 13
US-09-548-367D-64
; Sequence 64, Application US/09548367D
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT FILING DATE: 2000-04-12
; PRIORITY NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide

US-09-548-367D-64
Query Match 50.0%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 6 DAEFR 10

; APPLICANT: Kapur, Ravi
 ; TITLE OF INVENTION: A System for Cell Based Screening
 ; FILE REFERENCE: 97-022-11
 ; CURRENT APPLICATION NUMBER: US/09/513,783A
 ; CURRENT FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 92
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: b-Secretase
 ; OTHER INFORMATION: substrate recognition sequence
 ; US-09-513-783A-92

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Best Local Similarity	100.0%	Pred. No.	2e+05;	
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	DAEF 4			
Db 1	DAEF 4			

RESULT 14
 US-08-422-333-7
 ; Sequence 7, Application US/08422333
 ; Patent No. 5912410
 ; GENERAL INFORMATION:
 ; APPLICANT: CORDELL, Barbara L.
 ; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
 ; THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scios, Inc.
 ; STREET: 2450 Bayshore Parkway
 ; CITY: Mountain View
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94043
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/422,333
 ; FILING DATE: 13-APR-1995
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Shearer, Peter R.
 ; REGISTRATION NUMBER: 28,117
 ; REFERENCE/DOCKET NUMBER: 21900-2B048.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 966-1550
 ; TELEFAX: (415) 968-2438
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-422-333-7

Query Match	40.0%	Score 4;	DB 2;	Length 5;
Best Local Similarity	100.0%	Pred. No.	2e+05;	
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	DAEF 4			
Db 2	DAEF 5			

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:10:05 ; Search time 11 3333 Seconds
 (without alignments)
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Title:	US-09-580-018-9
Perfect score:	10
Sequence:	1 DAEFRHDSGY 10
Scoring table:	OLIGO
Gapop 60.0 , Gapext 60.0	
Searched:	288829 seqs, 75613885 residues
Word size :	0
Total number of hits satisfying chosen parameters :	33473
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Maximum DB seq length: 10	

Post-processing: Listing first 45 summaries

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 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep;*
 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep;*
 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep;*
 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep;*
 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep;*
 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep;*
 9: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep;*
 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep;*
 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep;*
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 13: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep;*
 14: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	10	100.0	10 9	US-09-865-294-69
2	7	70.0	7 10	US-09-867-847-59
3	5	50.0	5 10	US-09-794-927-72
4	5	50.0	5 10	US-09-794-743-72
5	5	50.0	5 10	US-09-794-847-72
6	5	50.0	5 10	US-09-794-748-72
7	5	50.0	5 10	US-09-794-927-72
8	5	50.0	5 10	US-09-681-442-72
9	5	50.0	5 10	US-09-794-847-72
10	5	50.0	8 10	US-09-149-718-10
11	5	50.0	10 9	US-09-795-903A-4
12	5	50.0	10 9	US-09-795-903A-5
13	5	50.0	10 10	US-09-794-927-63
14	5	50.0	10 10	US-09-794-927-64
15	5	50.0	10 10	US-09-795-847-63
16	5	50.0	10 10	US-09-795-847-64
17	5	50.0	10 10	US-09-794-743-63
18	5	50.0	10 10	US-09-794-743-64
19	5	50.0	10 10	US-09-794-748-63

SUMMARYS

Score	Query Match	Best Local Similarity	Score 10;	DB 9;	Length 10;
8	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
9	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;

Score	Query Match	Best Local Similarity	Score 10;	DB 9;	Length 10;
10	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
11	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
12	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
13	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
14	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
15	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
16	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
17	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
18	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;
19	1 DAFFRHDSGY 10	100.0%;	Pred. No. 1.7e-05;	0;	Mismatches 0;

Score	Query Match	Best Local Similarity	Score 10;	DB 9;	Length 10;
20	5 50.0	50.0	10 10	US-09-794-748-64	
21	5 50.0	50.0	10 10	US-09-796-264-4	
22	5 50.0	50.0	10 10	US-09-796-264-5	
23	5 50.0	50.0	10 10	US-09-794-925-63	
24	5 50.0	50.0	10 10	US-09-794-925-64	
25	5 50.0	50.0	10 10	US-09-681-442-63	
26	5 50.0	50.0	10 10	US-09-681-442-64	
27	5 50.0	50.0	10 10	US-09-845-226-4	
28	5 50.0	50.0	10 10	US-09-845-226-5	
29	4 40.0	40.0	4 10	US-09-808-037-1	
30	4 40.0	40.0	6 10	US-09-808-037-7	
31	4 40.0	40.0	7 9	US-10-057-505-10	
32	4 40.0	40.0	8 10	US-09-794-927-67	
33	4 40.0	40.0	8 10	US-09-795-847-67	
34	4 40.0	40.0	8 10	US-09-794-743-67	
35	4 40.0	40.0	8 10	US-09-794-748-67	
36	4 40.0	40.0	8 10	US-09-794-925-67	
37	4 40.0	40.0	8 10	US-09-681-442-67	
38	4 40.0	40.0	9 10	US-09-836-184-8	
39	4 40.0	40.0	9 10	US-09-896-139-8	
40	4 40.0	40.0	9 10	US-09-835-843-8	
41	4 40.0	40.0	9 12	US-10-016-717-6	
42	3 30.0	30.0	4 9	US-10-029-191-10	
43	3 30.0	30.0	4 9	US-10-091-135-90	
44	3 30.0	30.0	4 9	US-09-848-616-88	
45	3 30.0	30.0	4 10	US-09-916-230-19	

ALIGNMENTS

Score	Query Match	Best Local Similarity	Score 10;	DB 9;	Length 10;
RESULT 1	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
US-09-805-294-69	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
Sequence 69, Application US/09865294	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; GENERAL INFORMATION:	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; APPLICANT: WANG, Chang Yi	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the prevention and treatment of Alzheimer's Disease	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; FILE REFERENCE: 1151-4167	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; CURRENT APPLICATION NUMBER: US/09/865, 294	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; CURRENT FILING DATE: 2001-05-25	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; NUMBER OF SEQ ID NOS: 76	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; SOFTWARE: PatentIn Ver. 2.0	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; SEQ ID NO: 69	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; LENGTH: 10	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; TYPE: PRT	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; ORGANISM: Homo sapiens	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
US-09-865-294-69	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;

Score	Query Match	Best Local Similarity	Score 10;	DB 9;	Length 10;
RESULT 2	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
US-09-867-847-5	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
Sequence 5, Application US/09867847	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; GENERAL INFORMATION:	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; APPLICANT: Chalifour, Robert	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; APPLICANT: Hebert, Lise	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; APPLICANT: Kong, Xiangqi	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; APPLICANT: Gervais, Francine	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASES	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; FILE REFERENCE: 1443-501 CIP	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; CURRENT APPLICATION NUMBER: 1443-501 CIP	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;
; CURRENT FILING DATE: 2001-09-20	1 DAFFRHDSGY 10	100.0%;	Score 10;	DB 9;	Length 10;

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; GENERAL INFORMATION:
;   APPLICANT: Gurney, Mark E.
;   APPLICANT: Bienkowski, Michael J.
;   APPLICANT: Heinrikson, Robert L.
;   APPLICANT: Parodi, Luis A.
;   APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;   SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OS-09-867-847-5

Query Match          70.0%; Score 7; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DAEFRID 7
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Db      1 DAEFRHD 7

RESULT 3
OS-09-794-927-5
; Sequence 72, Application US/09794927
; Patent No. US2010016324A1

; GENERAL INFORMATION:
;   APPLICANT: Gurney, Mark E.
;   APPLICANT: Bienkowski, Michael J.
;   APPLICANT: Heinrikson, Robert L.
;   APPLICANT: Parodi, Luis A.
;   APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;   SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OS-09-867-847-5

Query Match          70.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DAEFR 5
       |||||
Db      1 DAEFR 5

RESULT 5
US-09-794-743-72
; Sequence 72, Application US/09794743
; Patent No. US20010021391A1

; GENERAL INFORMATION:
;   APPLICANT: Gurney, Mark E.
;   APPLICANT: Bienkowski, Michael J.
;   APPLICANT: Heinrikson, Robert L.
;   APPLICANT: Parodi, Luis A.
;   APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;   SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OS-09-794-927-72

Query Match          50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 60/101, 594
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DAEFR 5
       |||||
Db      1 DAEFR 5

RESULT 4
US-09-795-847-72
; Sequence 72, Application US/09795847
; Patent No. US2010018205AA1

; GENERAL INFORMATION:
;   APPLICANT: Gurney, Mark E.
;   APPLICANT: Bienkowski, Michael J.
;   APPLICANT: Heinrikson, Robert L.
;   APPLICANT: Parodi, Luis A.
;   APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;   SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OS-09-795-847-5

Query Match          50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DAEFR 5
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Db      1 DAEFR 5

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-794-743-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 1 DAEFR 5

RESULT 6
US-09-794-748-72
; Sequence 72, Application US/09794748
; Patent No. US20020037315A1.
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6380JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIORITY APPLICATION NUMBER: 09/416,901
; PRIORITY FILING DATE: 1999-10-13
; PRIORITY APPLICATION NUMBER: 1999-09-23
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY APPLICATION NUMBER: 1999-09-23
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY APPLICATION NUMBER: 1999-09-23
; PRIORITY FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-794-748-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 1 DAEFR 5

RESULT 7
US-09-794-925-72
; Sequence 72, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; PRIORITY APPLICATION NUMBER: US/09/681,442
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; PRIORITY APPLICATION NUMBER: US/09/681,442
; PRIORITY FILING DATE: 2001-04-05
; PRIORITY FILING DATE: 1999-10-13
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-681-442-72

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFR 5
Db 1 DAEFR 5

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RESULT 9
US-09-972-475-36
; Sequence 36, Application US/09972475
; Patent No. US2002009817A1
; GENERAL INFORMATION:
; APPLICANT: Finsdels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHTE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-972-475-36

Query Match 50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.0e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-149-718-10
; Sequence 10, Application US/09149718
; Patent No. US2002104104A1
; GENERAL INFORMATION:
; APPLICANT: Dora K. Games, Dale B. Schenck, Lisa C. McConlogue,
; Peter A. Seubert, and Russell E. Rydel
; TITLE OF INVENTION: Method For Identifying Alzheimer's Disease
; Number Of Sequences: 10
; Correspondence Address:
; Addressee: Patrea L. Pabst
; Street: 2800 One Atlantic Center
; City: Atlanta
; State: GA
; Country: USA

Query Match 50.0%; Score 5; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 DAEFR 5
 Db 6 DAEFR 10

RESULT 12
 US-09-795-903A-5
 ; Sequence 5, Application US/09795903A
 ; Patent No. US2001064760A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Jordan J.N.
 ; APPLICANT: Lin, Xinli
 ; APPLICANT: Koeisch, Gerald
 ; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
 ; TITLE OF INVENTION: of Use Thereof
 ; FILE REFERENCE: OMRF 179
 ; CURRENT APPLICATION NUMBER: US/09/795,903A
 ; CURRENT FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 09/604,608
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: 60/168,060
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: 60/177,836
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 60/178,368
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: 60/210,292
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; US-09-795-903A-5

Query Match Score 5; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 DAEFR 5
 Db 6 DAEFR 10

RESULT 13
 US-09-794-927-63
 ; Sequence 63, Application US/09794927
 ; Patent No. US200106324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Blenkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
 ; TITLE OF INVENTION: THESEFOR
 ; FILE REFERENCE: 2B341/6280FG
 ; CURRENT APPLICATION NUMBER: US/09/794,927
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 09/416,101
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: US/09/794,927
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PC1/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 64
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; US-09-794-927-64

Query Match Score 5; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 DAEFR 5
 Db 6 DAEFR 10

RESULT 15
 US-09-795-847-63
 ; Sequence 63, Application US/09795847
 ; Patent No. US2001063208A1
 ; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yau, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: US\$S
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 23341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/415,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
us-09-795-847-63

Query Match 50.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 5; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

Qy 1 DAEFR 5
Db 6 DAEFR 10

Search completed: April 21, 2003, 12:13:36
Job time : 12.3333 secs

Run on:	April 21, 2003, 12:07:50 ; Search time 22 Seconds (without alignments) 93.658 Million cell updates/sec	17	2	20.0	8	2	Q8RSR3
Title:	ORIGO	18	2	20.0	8	4	Q9UJ50
Perfect score:	10	19	2	20.0	8	4	Q15901
Sequence:	1 AEFRHDSGYE 10	20	2	20.0	8	4	Q9Y4J4
Scoring table:	Gapop 60.0 , Gapext 60.0	21	2	20.0	8	4	Q16428
Searched:	671580 seqs 206047115 residues	22	2	20.0	8	4	Q60773
Word size :	0	23	2	20.0	8	5	Q94623
Total number of hits satisfying chosen parameters:	124	24	2	20.0	8	5	Q9TWH6
Minimum DB seq length: 0		25	2	20.0	8	6	Q9MYL5
Maximum DB seq length: 10		26	2	20.0	8	6	Q9GMH3
Post-processing: Listing first 45 summaries		27	2	20.0	8	6	Q28866
Database :	SPTREMBL_21:*	28	2	20.0	8	6	Q8WNS1
	1: sp_archaea:*	29	2	20.0	8	6	Q9BFC3
	2: sp_bacteria:*	30	2	20.0	8	6	Q9BFC2
	3: sp_fungi:*	31	2	20.0	8	6	Q9BFC1
	4: sp_invertebrate:*	32	2	20.0	8	6	Q9BFC0
	5: sp_mammal:*	33	2	20.0	8	6	Q9BFB4
	6: sp_mhc:*	34	2	20.0	8	6	Q9BFB3
	7: sp_organelle:*	35	2	20.0	8	6	Q9BFB9
	8: sp_phage:*	36	2	20.0	8	6	Q9BFB8
	9: sp_plant:*	37	2	20.0	8	6	Q9BFB7
	10: sp_rhodent:*	38	2	20.0	8	6	Q9BFB5
	11: sp_virus:*	39	2	20.0	8	6	Q9BFB2
	12: sp_vertebrate:*	40	2	20.0	8	6	Q9BFB1
	13: sp_unclassified:*	41	2	20.0	8	6	Q9BB0
	14: sp_virus:*	42	2	20.0	8	6	Q9FA9
	15: sp_bacteriaphage:*	43	2	20.0	8	6	Q9BFA8
	16: sp_archaea:*	44	2	20.0	8	6	Q9BFA7
	17: sp_archeap:*	45	2	20.0	8	6	Q9BFA7
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1	30.0	8	13	Q9PS69	Opps69 gallus gallus		
2	30.0	10	6	Q9TU33	Q9TU33 canis familiaris		
3	30.0	10	10	P81899	P81899 prunus dulcis		
4	30.0	10	12	Q9T1G8	Q9j1g8 tt virus		
5	20.0	7	2	Q47477	Q47477 escherichia coli		
6	20.0	7	4	Q15897	Q15897 homo sapiens		
7	20.0	7	6	Q28742	Q28742 orctolagus cuniculus		
8	20.0	7	8	Q98866	Q98866 spinacia olivacea		
9	20.0	8	2	Q68485	Q68485 klebsiella		
10	20.0	8	2	Q9XK1	Q9XK1 prochlorococcus		
11	20.0	8	2	Q9SD5	Q9S6d5 escherichia coli		
12	20.0	8	2	P72221	P72221 pseudomonas aeruginosa		
13	20.0	8	2	Q9RTT2	Q9rtt2 escherichia coli		
14	20.0	8	2	Q9R5R2	Q9r5r2 shigella dysenteriae		
15	20.0	8	2	Q9R3X0	Q9r3x0 planktothrix		
16	20.0	8	2	Q9R5L7	Q9r5l7 clostridium		
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description	8	
1	30.0	8	13	Q9PS69	Opps69 gallus gallus		
2	30.0	10	6	Q9TU33	Q9TU33 canis familiaris		
3	30.0	10	10	P81899	P81899 prunus dulcis		
4	30.0	10	12	Q9T1G8	Q9j1g8 tt virus		
5	20.0	7	2	Q47477	Q47477 escherichia coli		
6	20.0	7	4	Q15897	Q15897 homo sapiens		
7	20.0	7	6	Q28742	Q28742 orctolagus cuniculus		
8	20.0	7	8	Q98866	Q98866 spinacia olivacea		
9	20.0	8	2	Q68485	Q68485 klebsiella		
10	20.0	8	2	Q9XK1	Q9XK1 prochlorococcus		
11	20.0	8	2	Q9SD5	Q9S6d5 escherichia coli		
12	20.0	8	2	P72221	P72221 pseudomonas aeruginosa		
13	20.0	8	2	Q9RTT2	Q9rtt2 escherichia coli		
14	20.0	8	2	Q9R5R2	Q9r5r2 shigella dysenteriae		
15	20.0	8	2	Q9R3X0	Q9r3x0 planktothrix		
16	20.0	8	2	Q9R5L7	Q9r5l7 clostridium		
SEQUENCE							
Result No.	Score	Match	Length	DB ID	Description	8	
1	30.0	8	13	Q9PS69	Opps69 gallus gallus		
2	30.0	10	6	Q9TU33	Q9TU33 canis familiaris		
3	30.0	10	10	P81899	P81899 prunus dulcis		
4	30.0	10	12	Q9T1G8	Q9j1g8 tt virus		
5	20.0	7	2	Q47477	Q47477 escherichia coli		
6	20.0	7	4	Q15897	Q15897 homo sapiens		
7	20.0	7	6	Q28742	Q28742 orctolagus cuniculus		
8	20.0	7	8	Q98866	Q98866 spinacia olivacea		
9	20.0	8	2	Q68485	Q68485 klebsiella		
10	20.0	8	2	Q9XK1	Q9XK1 prochlorococcus		
11	20.0	8	2	Q9SD5	Q9S6d5 escherichia coli		
12	20.0	8	2	P72221	P72221 pseudomonas aeruginosa		
13	20.0	8	2	Q9RTT2	Q9rtt2 escherichia coli		
14	20.0	8	2	Q9R5R2	Q9r5r2 shigella dysenteriae		
15	20.0	8	2	Q9R3X0	Q9r3x0 planktothrix		
16	20.0	8	2	Q9R5L7	Q9r5l7 clostridium		
SEQUENCE							
Result No.	Score	Match	Length	DB ID	Description	8	
1	30.0	8	13	Q9PS69	Opps69 gallus gallus		
2	30.0	10	6	Q9TU33	Q9TU33 canis familiaris		
3	30.0	10	10	P81899	P81899 prunus dulcis		
4	30.0	10	12	Q9T1G8	Q9j1g8 tt virus		
5	20.0	7	2	Q47477	Q47477 escherichia coli		
6	20.0	7	4	Q15897	Q15897 homo sapiens		
7	20.0	7	6	Q28742	Q28742 orctolagus cuniculus		
8	20.0	7	8	Q98866	Q98866 spinacia olivacea		
9	20.0	8	2	Q68485	Q68485 klebsiella		
10	20.0	8	2	Q9XK1	Q9XK1 prochlorococcus		
11	20.0	8	2	Q9SD5	Q9S6d5 escherichia coli		
12	20.0	8	2	P72221	P72221 pseudomonas aeruginosa		
13	20.0	8	2	Q9RTT2	Q9rtt2 escherichia coli		
14	20.0	8	2	Q9R5R2	Q9r5r2 shigella dysenteriae		
15	20.0	8	2	Q9R3X0	Q9r3x0 planktothrix		
16	20.0	8	2	Q9R5L7	Q9r5l7 clostridium		
SEQUENCE							
Result No.	Score	Match	Length	DB ID	Description	8	
1	30.0	8	13	Q9PS69	Opps69 gallus gallus		
2	30.0	10	6	Q9TU33	Q9TU33 canis familiaris		
3	30.0	10	10	P81899	P81899 prunus dulcis		
4	30.0	10	12	Q9T1G8	Q9j1g8 tt virus		
5	20.0	7	2	Q47477	Q47477 escherichia coli		
6	20.0	7	4	Q15897	Q15897 homo sapiens		
7	20.0	7	6	Q28742	Q28742 orctolagus cuniculus		
8	20.0	7	8	Q98866	Q98866 spinacia olivacea		
9	20.0	8	2	Q68485	Q68485 klebsiella		
10	20.0	8	2	Q9XK1	Q9XK1 prochlorococcus		
11	20.0	8	2	Q9SD5	Q9S6d5 escherichia coli		
12	20.0	8	2	P72221	P72221 pseudomonas aeruginosa		
13	20.0	8	2	Q9RTT2	Q9rtt2 escherichia coli		
14	20.0	8	2	Q9R5R2	Q9r5r2 shigella dysenteriae		
15	20.0	8	2	Q9R3X0	Q9r3x0 planktothrix		
16	20.0	8	2	Q9R5L7	Q9r5l7 clostridium		
SEQUENCE							
Result No.	Score	Match	Length	DB ID	Description	8	
1	30.0	8	13	Q9PS69	Opps69 gallus gallus		
2	30.0	10	6	Q9TU33	Q9TU33 canis familiaris		
3	30.0	10	10	P81899	P81899 prunus dulcis		
4	30.0	10	12	Q9T1G8	Q9j1g8 tt virus		
5	20.0	7	2	Q47477	Q47477 escherichia coli		
6	20.0	7	4	Q15897	Q15897 homo sapiens		
7	20.0	7	6	Q28742	Q28742 orctolagus cuniculus		
8	20.0	7	8	Q98866	Q98866 spinacia olivacea		
9	20.0	8	2	Q68485	Q68485 klebsiella		
10	20.0	8	2	Q9XK1	Q9XK1 prochlorococcus		
11	20.0	8	2	Q9SD5	Q9S6d5 escherichia coli		
12	20.0	8	2	P72221	P72221 pseudomonas aeruginosa		
13	20.0	8	2	Q9RTT2	Q9rtt2 escherichia coli		
14	20.0	8	2	Q9R5R2	Q9r5r2 shigella dysenteriae		
15	20.0	8	2	Q9R3X0	Q9r3x0 planktothrix		
16	20.0	8	2	Q9R5L7	Q9r5l7 clostridium		
SEQUENCE							
Result No.	Score	Match	Length	DB ID	Description	8	
1	30.0	8	13	Q9PS69	Opps69 gallus gallus		
2	30.0	10	6	Q9TU33	Q9TU33 canis familiaris		
3	30.0	10	10	P81899	P81899 prunus dulcis		
4	30.0	10	12	Q9T1G8	Q9j1g8 tt virus		
5	20.0	7	2	Q47477	Q47477 escherichia coli		
6	20.0	7	4	Q15897	Q15897 homo sapiens		
7	20.0	7	6	Q28742	Q28742 orctolagus cuniculus		
8	20.0	7	8	Q98866	Q98866 spinacia olivacea		
9	20.0	8	2	Q68485	Q68485 klebsiella		
10	20.0	8	2	Q9XK1	Q9XK1 prochlorococcus		
11	20.0	8	2	Q9SD5	Q9S6d5 escherichia coli		
12	20.0	8	2	P72221	P72221 pseudomonas aeruginosa		
13	20.0	8	2	Q9RTT2	Q9rtt2 escherichia coli		
14	20.0	8	2	Q9R5R2	Q9r5r2 shigella dysenteriae		
15	20.0	8	2	Q9R3X0	Q9r3x0 planktothrix		
16	20.0	8	2	Q9R5L7	Q9r5l7 clostridium		
SEQUENCE							
Result No.	Score	Match	Length	DB ID	Description	8	
1	30.0	8	13	Q9PS69	Opps69 gallus gallus		
2	30.0	10	6	Q9TU33	Q9TU33 canis familiaris		
3	30.0	10	10	P81899	P81899 prunus dulcis		
4	30.0	10	12	Q9T1G8	Q9j1g8 tt virus		
5	20.0	7	2	Q47477	Q47477 escherichia coli		
6	20.0	7	4	Q15897	Q15897 homo sapiens		
7	20.0	7	6	Q28742	Q28742 orctolagus cuniculus		
8	20.0	7	8	Q98866	Q98866 spinacia olivacea		
9	20.0	8	2	Q68485	Q68485 klebsiella		
10	20.0	8	2	Q9XK1	Q		

DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)					RESULT 4
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)					
BRCA1		(Fragment).					
GN							
OS	Canis familiaris (Dog).						
Eukaryota;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia;	Eutheria; carnivora; Fissipedia; Canidae; Canis;						
NCBL_TaxID=9615;							
[1]							
RN	SEQUENCE FROM N.A.						
RX	MEDLINE=20154965; PubMed=10690375;						
RX	Gray L.S., Yuzbasyan-Gurkan V.;	"A single nucleotide (T-->G) polymorphism within intron 23 of the canine BRCA1 gene."					
RT	Anim. Genet. 31:76-77(2000).						
EMBL;	AFF159258;	AAD56389.1;					
DR	NON_TER 1 1						
FT	NON_TER 10 10						
SEQUENCE	10 AA; 1164 MW;	2AB89C65BAA801B3 CRC64;					
Query Match	Score 30.0%; Best Local Similarity 100.0%; Matches 3;	Score 3 DB 6; Pred. No. 3.3e+03; Conservative 0; Mismatches 0;	Length 10;				
Qy	6 DSG 8	0; Gaps 0;	Indels 0;				
Db	6 DSG 8						
REVERSE 3							
PB1899	PB1899	PRELIMINARY;	PRT;	10 AA.			RESULT 5
ID	PB1899;						
DT	01-MAR-2001	(TREMBLrel. 16, Created)					
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)					
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)					
DE	Peptide N4-(N-acetyl-beta-D-glucosaminyl)asparagine amidase A, large chain (Subunit A) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-glycosidase) (N-glycanase) (Fragment).						
DE	Prunus dulcis (Almond) (Prunus amygdalus).						
OS	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; audicoryledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.						
NCBL_TaxID=3755;							
[1]							
RN	SEQUENCE, AND CHARACTERIZATION.						
RX	PubMed=523720;						
RX	Altmann F., Paschinger K., Dalik T., Vorauer K.;	"Characterisation of Peptidase-N4 (N-acetyl-beta-D-glucosaminyl)asparagine amidase A and its N-glycans."					
RT	Eur. J. Biochem. 252:118-123 (1998).						
-1-	CATALYTIC ACTIVITY:	HYDROLYSIS OF AN N4-(ACETYL-BETA-D-GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE CONTAINING AN ASPARTIC RESIDUE.					
-1-	SUBUNIT:	HETERODIMER OF A LARGE AND A SMALL CHAIN.					
-1-	PTM:	IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-DEGLYCOSYLATION.					
CC	-1- MASS SPECTROMETRY: MW=54182; METHOD=MALDI-MS.						
CC	KW Hydrolase; Glycoprotein.						
CC	NON_TER 10 10						
SEQUENCE	10 AA; 1106 MW;	95f6BF65B1FB5865 CRC64;					
SQ	Query Match	Score 30.0%; Best Local Similarity 100.0%; Matches 3;	Score 3 DB 10; Pred. No. 3.3e+03; Conservative 0; Mismatches 0;	Length 10;			RESULT 6
Qy	1 AE 2	0; Gaps 0;	Indels 0;				
Db	1 AE 2						

01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE (clone XP6A11A) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 Chinault C.A., Lindsay E.A., Zhao Z.-Y.,
 Coobaugh M.I., Chinault C.A., Baldini A.,
 Caskey C.T H.;
 RT *Isolation of chromosome-specific genes by reciprocal probing of
 arrayed cDNAs and cosmid libraries.";
 RL Hum Mol Genet 0:0(0:1995).
 DR EMBL; L32077; AAA73887.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;
 Query Match 20.0%; Score 2; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AE 2
 Db 5 AE 6
 RESULT 7
 Q28742 PRELIMINARY; PRT; 7 AA.
 AC Q28742;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Alpha-myosin heavy chain (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagids.
 NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-842219901; PubMed=6328491;
 RA Friedman D.J., Umehara P.K., Sinha A.M., Hsu H.-J., Jokovicic S.,
 Rabinowitz M.;
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-
 ventricular myosin heavy chains";
 PROC Natl Acad Sci U.S.A. 81:3044-3048(1984).
 DR EMBL; K01680; AAA31415.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;
 Query Match 20.0%; Score 2; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 HD 6
 Db 4 HD 5
 RESULT 8
 Q98866 PRELIMINARY; PRT; 7 AA.
 AC Q98866;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE cytochrome b/f subunit IV (Fragment).
 OS Spinacia olerecea (Spinach).
 OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86120333; PubMed=3003688;
 RA Sijben-Muelier G., Hallieck R.B., Alt J., Westhoff P., Herrmann R.G.;
 RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal RNA;
 RT Protein S11 and RNA polymerase alpha-subunit.";
 RL Nucleic Acids Res. 14:1029-1044(1986).
 DR EMBL; X03496; CAA27215.1; -.
 KW Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;
 Query Match 20.0%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 FR 4
 Db 2 FR 3
 RESULT 9
 Q68485 PRELIMINARY; PRT; 8 AA.
 ID Q68485;
 AC 068485;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update).
 DE Aminoglycoside 3'-O-nucleotidytransferase (Fragment).
 GN ADA1.
 OS Klebsiella pneumoniae.
 OG Plasmid pKO1000.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE-98287600; PubMed=9624504;
 RA Centron D., Roy P.-H.;
 RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene
 aac(6')-Iq from the integron of a natural multiresistance plasmid.";
 RL Antimicrob Agents Chemother. 42:1506-1508(1998).
 DR EMBL; AF047556; AAC25501.1; -.
 KW Plasmid; Transferase.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64;
 Query Match 20.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AE 2
 Db 3 AE 4
 RESULT 10
 Q9X3K1 PRELIMINARY; PRT; 8 AA.
 ID Q9X3K1;
 AC Q9X3K1;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE Cytochrome b (Fragment).
 GN PETB.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.

NCBI_TaxID=1220;			
RN [1]	SEQUENCE FROM N.A.		
RP Urbach E., Chisholm S.W.;	"Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";		
RA RT	Limnol. Oceanogr. 43:1615-1630 (1998).		
DR EMBL; AFO0193; AAD3233.1; -.			
FT NON_TER 1	SEQUENCE 8 AA; 799 MW;	1037685B72866D3 CRC64;	
SQ	Best Local Similarity 100.0%; Pred. No. 6.7e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 2; DB 2; Length 8;	
QY 7 SG 8	Db 5 SG 6	QY 1 AE 2	
Db 7 AE 8	Db 7 AE 8	Db 7 AE 8	
RESULT 11			
Q9SSD5	PRELIMINARY;	PRT;	
ID Q9SSD5	8 AA.	8 AA.	
AC			
Q9SSD5			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
PUTATIVE IS0 transposase (Fragment).			
OS Escherichia coli.			
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC Escherichia.			
OX NCBI_TaxID=562;			
RN	SEQUENCE FROM N.A.		
RP			
RC STRAIN=Q295B;			
RX MEDLINE-91194747; PubMed=10094716;			
RA Paine A., Drummond J., Whitfield C.;	"Conserved organization in the cps gene clusters for expression of biosynthesis coli group I K antigens: relationship to the colanic acid locus and the cps genes from Klebsiella pneumoniae."		
RT	J. Bacteriol. 181:2307-2313 (1999).		
RL DR	EMBL; AF118231; AAD30008.1; -.		
FT NON_TER 8	SEQUENCE 8 AA; 1011 MW;	F21DC1A9D1B41406 CRC64;	
SQ	Best Local Similarity 100.0%; Pred. No. 6.7e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 2; DB 2; Length 8;	
QY 1 AE 2	Db 7 AE 8	QY 1 AE 2	
Db 7 AE 8	Db 7 AE 8	Db 7 AE 8	
RESULT 12			
P72221	PRELIMINARY;	PRT;	
ID P72221;	8 AA.	8 AA.	
AC			
P72221;			
DT 01-FEB-1997 (TREMBLrel. 02, Created)			
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE Alginate lyase (Fragment).			
GN ALY.			
OS Pseudomonas sp. (strain OS-ALG-9).			
OC Bacteria; Proteobacteria.			
OX NCBI_TaxID=86038;			
RN	SEQUENCE FROM N.A.		
RP STRAIN=OS-ALG-9;			
RC Fujiyama K.;			
RA Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.			
RN [2]	SEQUENCE FROM N.A.		
RP			
NCBI_TaxID=622.			
OX			
RESULT 13			
Q9RRT2	PRELIMINARY;	PRT;	
ID Q9RRT2	8 AA.	8 AA.	
AC			
Q9RRT2			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE Hypothetical 1.0 kDa protein (Fragment).			
GN YOFG.			
OS Escherichia coli.			
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC Escherichia.			
OX NCBI_TaxID=562;			
RP	SEQUENCE FROM N.A.		
RC STRAIN=K12;			
RX MEDLINE-97051202; PubMed=8905232;			
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Kajihara M., Kanai K., Kashimoto K.,			
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,			
RA Kimura S., Kitagawa M., Makino K., Nasuda S., Miki T., Mizobuchi K.,			
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,			
RA Sampi G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,			
RA Yano M., Horiuchi T.,			
RT "A 718 kb DNA Sequence of Escherichia coli K-12 Genome Corresponding to the 12.7-28.0 min Region on the Linkage Map.";			
RT DR DNA Res. 3:137-155 (1996);			
DR EMBL; D90705; BA35310.1;			
KW Hypothetical protein.			
FT NON_TER 1	SEQUENCE 8 AA; 964 MW;	DF133B1DD004B476A CRC64;	
SQ	Best Local Similarity 100.0%; Pred. No. 6.7e-05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 2; DB 2; Length 8;	
QY 1 AE 2	Db 7 AE 8	QY 1 AE 2	
Db 7 AE 8	Db 7 AE 8	Db 7 AE 8	
RESULT 14			
Q9RRZ2	PRELIMINARY;	PRT;	
ID Q9RRZ2	8 AA.	8 AA.	
AC			
Q9RRZ2			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE 31,000 DA product of ORFB (Fragment).			
OS Shigella dysenteriae.			
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC Shigella.			
OX NCBI_TaxID=622.			

RN [1]
 RP SEQUENCE.
 RX MEDLINE=92085266; PubMed=1660923;
 RA Polard P., Prete M.F., Chandler M., Fayet O.;
 RT "Programmed translational frameshifting and initiation at an AUU codon
 in gene expression of bacterial insertion sequence IS911.";
 RL J. Mol. Biol. 222:465-477(1991).
 FT NON_TER 8
 SQ SEQUENCE 8 AA: 902 MW: FEEDCATB586AE336 CRC64;

RESULT 15
 Q9R3X0 PRELIMINARY; PRT; 8 AA.
 ID Q9R3X0
 AC Q9R3X0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
 DE (Fragment).
 GN PBCI.
 OS Planktothrix rubescens.
 OC Bacteria; Cyanobacteria; Oscillatoriaceae; Planktothrix.
 OX NCBI_TaxID=59512;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BC-PLA 9316, AND BC-PLA 9303;
 RX MEDLINE=0005589; PubMed=1053797;
 RA Beard S.J., Handley B.A., Hayes P.K., Walsby A.E.;
 RT "The diversity of gas vesicle genes in *Planktothrix* rubescens from
 Lake Zurich." 145:2757-2768(1999).
 RL Microbiology 145:2757-2768(1999).
 DR AJ132249; CAB59537.1;
 DR AJ132248; CAB59534.1;
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA: 957 MW: 33DIAAA685BB19CB CRC64;

 Query Match 20.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EF 3
 Db 1 EF 2

 Search completed: April 21, 2003, 12:11:40
 Job time : 23 secs

GenCore version 5.1.4_D5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:08:10 ; search time 11.6667 Seconds
 (without alignments)
 82.401 Million cell updates/sec

Perfect score: 10 US-09-580-018-10
 Sequence: 1 AEFRHDSGYE 10

Scoring table: OLIIGO Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : PIR_73;*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	3	30.0	5	2	A26830		mitosis inhibiting ribosomal protein peptide N-(N-acet
2	3	30.0	8	2	A26830		Ig heavy chain in CRD
3	3	30.0	10	2	PT0243		T-cell receptor be
4	3	30.0	10	2	PT0215		T-cell receptor be
5	3	30.0	10	2	PH0900		T-cell receptor be
6	3	30.0	10	2	PT0571		T-cell receptor be
7	2	20.0	3	3	PT0571		globulin IV alpha
8	2	20.0	4	2	S09478		T-cell receptor be
9	2	20.0	4	2	PT0633		T-cell receptor be
10	2	20.0	4	2	PT0711		T-cell receptor be
11	2	20.0	4	2	PT0698		T-cell receptor be
12	2	20.0	4	2	PT0677		T-cell receptor be
13	2	20.0	4	2	PT0706		T-cell receptor be
14	2	20.0	4	2	PT0675		T-cell receptor be
15	2	20.0	4	2	PT0566		copper resistance
16	2	20.0	5	2	A41225		copper resistance
17	2	20.0	5	2	B41225		major protein anti
18	2	20.0	5	2	D60274		acid proteinase li
19	2	20.0	5	2	B37988		fulicin - giant Af
20	2	20.0	5	2	A44692		19 kappa chain V-I
21	2	20.0	5	2	JT0520		synaptosomal assoc
22	2	20.0	5	2	D44823		T-cell receptor be
23	2	20.0	5	2	PT0512		T-cell receptor be
24	2	20.0	5	2	PT0600		T-cell receptor be
25	2	20.0	5	2	PT0608		T-cell receptor be
26	2	20.0	5	2	PT0669		T-cell receptor be
27	2	20.0	5	2	PT0553		T-cell receptor be
28	2	20.0	5	2	PT0538		T-cell receptor be
29	2	20.0	5	2	PT0540		T-cell receptor be

ALIGNMENTS

RESULT 1

A26830

mitosis inhibiting peptide - mouse
 C;Species: Mus musculus (house mouse)C;Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C;Accession: A26830
 R;Reichelt, K.; Elvio, K.; Edminson, P.D.Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
 A;Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
 A;Reference number: A26830; PMID:3619940

A;Accession: A26830

A;Molecule type: protein

A;Residues: 1-5 <REI>

C;Superfamily: unassigned animal peptides

F;1/Modified site: Pyrrolidine carboxylic acid (Gln) #status experimental
 Query Match Score 3: DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

Db

6 DSG 8
 111
 3 DSG 5ribosomal protein YmS-B, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
 C;Species: Saccharomyces cerevisiae
 C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997C;Accession: S78036
 R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Harfurth, E.; Wit
 Eur. J. Biochem. 245, 449-456, 1997
 A;Title: Identification and characterization of the genes for mitochondrial ribosomalA;Reference number: S78018; PMID:97295614; PMID:9151978
 A;Accession: S78036
 A;Molecule type: protein
 A;Residues: 1-8 <KIR>
 C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match Score 3: DB 2; Length 8;

Qy Db

6 DSG 8
 111
 6 DSG 8Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Query Match Score 3: DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Query Match Score 3: DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 A59272

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain

N; Alternate names: peptide N-glycosidase

C; Species: Prunus dulcis var. sativa (sweet almond)

C; Date: 19-May-2000 #sequence_revision 19-May-2000

C; Accession: A59272

R; Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

Eur. J. Biochem. 252, 118-123, 1998

A; Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase

A; Reference number: A59272; PMID:9523720

A; Accession: A59272

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-10 <ALT>

C; Keywords: hydrolase

Query Match Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 3; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 7 SGV 9

Db 3 SGV 5

RESULT 4

PT0243 Ig heavy chain CRD3 region (clone 2-103A) - human (fragment)

C; Species: Homo sapiens (man)

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993

C; Accession: PT0243

R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A; Reference number: PT0243

A; Experimental source: B lymphocyte

C; Keywords: heterotrimer; immunoglobulin

Query Match Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 3; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 7 SGV 9

Db 7 SGV 9

RESULT 5

PT0215 T-cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991

C; Accession: PT0215

R; Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A; Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted

A; Reference number: PT0215; PMID:1902501

A; Accession: PT0215

A; Molecule type: mRNA

A; Residues: 1-10 <NKR>

C; Keywords: T-cell receptor

Query Match Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 3; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 8 GYE 10

Db 5 GYE 7

RESULT 6

PT0900 T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)

C; Species: Rattus norvegicus (Norway rat)

C; Date: 09-Oct-1992 #sequence_revision 09-Oct-1992

C; Accession: PH0900

R; Gold, D.P.; Offner, H.; Sun, D.; Vandembark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A; Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle

A; Reference number: PH0891; PMID:9207837; MUID:1836012

A; Accession: PH0891

A; Molecule type: mRNA

A; Residues: 1-10 <GOL>

C; Keywords: T-cell receptor

Query Match Score 30.0%;

Best Local Similarity 100.0%;

Matches 3; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 6 DSG 8

Db 5 DSG 7

RESULT 7

PT0571 T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001

C; Accession: PT0571

R; Fenney, A.J.

J. Exp. Med. 174, 115-124, 1991

A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A; Reference number: PT0509; PMID:91277601; PMID:1711558

A; Accession: PT0571

A; Status: translation not shown

A; Molecule type: mRNA

A; Residues: 1-3 <SPE>

C; Experimental source: day 19 fetal thymus, strain BALB/C

C; Keywords: T-cell receptor

Query Match Score 30.0%;

Best Local Similarity 100.0%;

Matches 2; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 7 SG 8

Db 2 SG 3

RESULT 8

S09478 globulin IV alpha subunit gamma chain, seed - curcubit (fragment)

N; Alternative names: 11S globulin alpha subunit gamma chain

C; Species: Cucurbita sp. (curcubit)

C; Date: 21-Nov-1993 #sequence_revision 08-Nov-1996

C; Accession: S09478

R; Ohmura, M.; Hara, I.; Matsubara, H.

Plant Cell Physiol. 21, 157-167, 1980

A; Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic a

A; Reference number: S09066

A; Accession: S09478

A; Molecule type: protein

A; Residues: 1-4 <CHM>

Query Match Score 20.0%;

Best Local Similarity 100.0%;

Matches 2; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 8 GY 9

Db 3 GY 4

RESULT 9
 PR0633 T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0633
 R;Feeney, A. J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0633
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: newborn thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query	Match	Score	DB	Length	4;	
Matches	2;	100.0%	Pred.	No.	2.8e+05;	
Qy	7 SG 8		Mismatches	0;	Indels	0;
Db	1 2 SG 3		Gaps	0;		

RESULT 10
 PR0711 T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0674; PR0678; PT0570; PT0711; PT0710
 R;Feeney, A. J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0607
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEL>
 A;Experimental source: newborn thymus, strain BALB/c, 120-2J
 A;Accession: PT0674
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
 A;Accession: PT0678
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FE3>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
 A;Accession: PT0711
 A;Status: translation not shown
 C;Keywords: T-cell receptor

Query	Match	Score	DB	Length	4;	
Matches	2;	100.0%	Pred.	No.	2.8e+05;	
Qy	7 SG 8		Mismatches	0;	Indels	0;
Db	1 2 SG 3		Gaps	0;		

RESULT 11
 PR0638 T-cell receptor beta chain V-D-J region (126-1AH) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997
 C;Accession: PR0546; PR0698; PT0583
 R;Feeney, A. J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PR0509; MUID:91277601; PMID:1711558
 A;Accession: PR0546
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AH
 A;Accession: PR0698
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FE2>
 A;Experimental source: newborn thymus, strain BALB/c, 135-1BP
 A;Accession: PR0583
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FE3>
 A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2C
 C;Keywords: T-cell receptor

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Matches	2;	100.0%	Pred.	No.	2.8e+05;	
Qy	7 SG 8		Mismatches	0;	Indels	0;
Db	1 2 SG 3		Gaps	0;		

RESULT 12
 PR0677 T-cell receptor beta chain V-D-J region (126-1BG) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0677
 R;Feeney, A. J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0607
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1H
 A;Accession: PR0677
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1BH
 A;Accession: PR0706
 A;Status: translation not shown
 C;Keywords: T-cell receptor

Query	Match	Score	DB	Length	4;	
Matches	2;	100.0%	Pred.	No.	2.8e+05;	
Qy	7 SG 8		Mismatches	0;	Indels	0;
Db	1 2 SG 3		Gaps	0;		

RESULT 13
 PR0706 T-cell receptor beta chain V-D-J region (135-1DU) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0706
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; PMID:91277601; PMID:1711558
 A;Accession: PT0706
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FEE>
 C;Keywords: T-cell receptor

Search completed: April 21, 2003, 12:12:21
 Job time : 11.6667 secs

Query Match Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 SG 8
 |
 Db 2 SG 3

RESULT 14
 PT0675
 T-cell receptor beta chain V-D-J region (140-1AC) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0675
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; PMID:91277601; PMID:1711558
 A;Accession: PT0675
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/C
 C;Keywords: T-cell receptor

Query Match Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 SG 8
 |
 Db 2 SG 3

RESULT 15
 PT0566
 T-cell receptor beta chain V-D-J region (141-1CH) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0566
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; PMID:91277601; PMID:1711558
 A;Accession: PT0566
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 19 fetal thymus, strain BALB/C
 C;Keywords: T-cell receptor

Query Match Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 SG 8
 |
 Db 2 SG 3



GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:10:05 ; Search time 11:3333 Seconds
 (without alignments)
 66.718 Million cell updates/sec

Title: US-09-580-018-10
 Perfect score: 10
 Sequence: 1 AEFRHDSGY 10

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 75613885 residues

Word size : 0

Total number of hits satisfying chosen parameters: 33473

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6_ptodata/2/pubpaas/US05_NEW_PUB.pep;*
3: /cgn2_6_ptodata/2/pubpaas/US05_NEW_PUB.pep;*
4: /cgn2_6_ptodata/2/pubpaas/US06_PUBCOMB.pep;*
5: /cgn2_6_ptodata/2/pubpaas/US07_PUBCOMB.pep;*
6: /cgn2_6_ptodata/2/pubpaas/US07_PUBCOMB.pep;*
7: /cgn2_6_ptodata/2/pubpaas/PCUTS_PUBCOMB.pep;*
8: /cgn2_6_ptodata/2/pubpaas/PCUTS_PUBCOMB.pep;*
9: /cgn2_6_ptodata/2/pubpaas/US08_PUBCOMB.pep;*
10: /cgn2_6_ptodata/2/pubpaas/US09_NEW_PUB.pep;*
11: /cgn2_6_ptodata/2/pubpaas/US10_NEW_PUB.pep;*
12: /cgn2_6_ptodata/2/pubpaas/US10_PUBCOMB.pep;*
13: /cgn2_6_ptodata/2/pubpaas/US60_NEW_PUB.pep;*
14: /cgn2_6_ptodata/2/pubpaas/US60_PUBCOMB.pep;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	90.0	10	9 US-09-865-294-69	Sequence 69, Appl
2	6	60.0	7	10 US-09-867-847-5	Sequence 5, Appl
3	5	50.0	5	10 US-09-972-475-36	Sequence 36, Appl
4	4	40.0	4	10 US-09-808-037-1	Sequence 72, Appl
5	4	40.0	5	10 US-09-794-927-72	Sequence 72, Appl
6	4	40.0	5	10 US-09-795-847-72	Sequence 72, Appl
7	4	40.0	5	10 US-09-794-743-72	Sequence 72, Appl
8	4	40.0	5	10 US-09-794-748-72	Sequence 72, Appl
9	4	40.0	5	10 US-09-794-925-72	Sequence 72, Appl
10	4	40.0	5	10 US-09-681-442-72	Sequence 72, Appl
11	4	40.0	6	10 US-09-808-037-7	Sequence 7, Appl
12	4	40.0	8	10 US-09-149-718-10	Sequence 10, Appl
13	4	40.0	10	9 US-09-795-903A-4	Sequence 4, Appl
14	4	40.0	10	9 US-09-795-903A-5	Sequence 5, Appl
15	4	40.0	10	10 US-09-794-927-63	Sequence 63, Appl
16	4	40.0	10	10 US-09-794-927-64	Sequence 64, Appl
17	4	40.0	10	10 US-09-795-847-63	Sequence 63, Appl
18	4	40.0	10	10 US-09-795-847-64	Sequence 64, Appl
19	4	40.0	10	10 US-09-794-743-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
 US-09-865-294-69
 ; Sequence 69, Application US-09865294
 ; Publication No. US20030068325A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Chang Yi
 ; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the prevention and treatment of Alzheimer's Disease
 ; FILE REFERENCE: 1151-4167
 ; CURRENT APPLICATION NUMBER: US-09-865, 294
 ; CURRENT FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 69
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-865-294-69

Query Match 90.0%; Score 9; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 US-09-867-847-5
 ; Sequence 5, Application US-09867847
 ; Patent No. US20020094335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chalifour, Robert
 ; APPLICANT: Hebert, Lise
 ; APPLICANT: Kong, Xiangji
 ; APPLICANT: Gervais, Francine
 ; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASES
 ; FILE REFERENCE: 1444-501 CIP
 ; CURRENT APPLICATION NUMBER: US-09-867, 847
 ; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/1168,594
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/724,812
 ; PRIOR FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 5
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
 ; OTHER INFORMATION: or peptidomimetics
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 Query Match 60.0% Score 6; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFRHD 6
 Db 2 AEFRHD 7
 ;
 RESULT 3 US-09-972-475-36
 ; Sequence 36, Application US/09972475
 ; Patent No. US2000098173A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Findeis, Mark A. et al.
 ; TITLE OF INVENTION: Modulators of Amyloid Aggregation
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/972,475
 ; FILING DATE: 04-Oct-2001
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/617,267
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: USSN 08/475,579
 ; FILING DATE: 07-JUN-1995
 ; APPLICATION NUMBER: USSN 08/548,998
 ; FILING DATE: 27-OCT-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeConti, Giulio A.
 ; REGISTRATION NUMBER: 31,503
 ; REFERENCE/DOCKET NUMBER: PPI-002CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 ; FRAGMENT TYPE: Internal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
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 Query Match 50.0% Score 5; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;
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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 HDSGY 9
 Db 1 HDSGY 5
 ;
 RESULT 4 US-09-808-037-1
 ; Sequence 1, Application US/09808037
 ; Patent No. US2005231A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SOLOMON, Bekah
 ; APPLICANT: HANAN, Eilat
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
 ; FILE REFERENCE: NEUROLOGICAL DISEASES AND DISORDERS
 ; CURRENT APPLICATION NUMBER: US/09/808,037
 ; CURRENT FILING DATE: 2001-03-15
 ; PRIOR APPLICATION NUMBER: US 09/629,971
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: US 09/473,653
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: US 60/152,417
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 1
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 ; US-09-808-037-1
 ; Query Match 40.0% Score 4; DB 10; Length 4;
 ; Best Local Similarity 100.0%; Pred. No. 2.6e+05;
 ; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 QY 2 EFRH 5
 Db 1 EFRH 4
 ;
 RESULT 5 US-09-794-327-72
 ; Sequence 72, Application US/09794927
 ; Patent No. US200101632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Blenkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Van, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 ; TITLE OF INVENTION: USES
 ; FILE REFERENCE: 28341/62B0PG
 ; CURRENT APPLICATION NUMBER: US/09/794,927
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 72

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; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-927-72

Query Match Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AEFR 5

RESULT 6
US-09-795-847-72
Sequence 72, Application US/09795847
; Patent No. US20100218208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

Query Match Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFR 4
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Db 2 AEFR 5

RESULT 7
US-09-794-743-72
Sequence 72, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

Query Match Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Software: PatentIn Ver. 2.0

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Qy 1 AEFR 4 ; PRIORITY FILING DATE: 1998-09-24
 1111 ; NUMBER OF SEQ ID NOS: 73
 Db 2 AEFR 5 ; SOFTWARE: PatentIn Ver. 2.0

RESULT 9
US-09-794-925-72 ; Sequence 72, Application US/09794925
 ; GENERAL INFORMATION:
 ; PATENT NO. US20020064819A1
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Bleirkowski, Michael J.
 ; APPLICANT: Heiriksson, Robert L.
 ; APPLICANT: Paredi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
 ; FILE REFERENCE: 28341/6280H1
 ; CURRENT APPLICATION NUMBER: US/09/794,925
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
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 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic

Qy 1 AEFR 4 ; PRIORITY FILING DATE: 1998-09-24
 1111 ; NUMBER OF SEQ ID NOS: 73
 Db 2 AEFR 5 ; SOFTWARE: PatentIn Ver. 2.0

RESULT 11
US-09-808-037-7 ; Sequence 7, Application US/09808037
 ; Patent No. US2002005231A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HANAN, Eilat
 ; APPLICANT: SOLOMON, Beka
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
 ; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
 ; FILE REFERENCE: SOLOMON-2D
 ; CURRENT APPLICATION NUMBER: US/09/808,037
 ; CURRENT FILING DATE: 2001-03-15
 ; PRIOR APPLICATION NUMBER: 09/629,971
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: US 09/473,653
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: US 60/152,417
 ; PRIOR FILING DATE: 1999-09-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 7
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide

Qy 2 EFRH 5 ; PRIORITY FILING DATE: 1998-09-24
 1111 ; NUMBER OF SEQ ID NOS: 73
 Db 3 EFRH 6 ; SOFTWARE: PatentIn Ver. 2.0

RESULT 12
US-09-681-442-72 ; Sequence 10, Application US/09149718
 ; Patent No. US2002010410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dora K. Games, Dale B. Schenk, Lisa C. McConlogue,
 ; APPLICANT: Peter A. Seubert, and Russell E. Rydel
 ; TITLE OF INVENTION: Method For Identifying Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center
 ; STREET: 1201 West Peachtree Street
 ; CITY: Atlanta
 ; STATE: GA

RESULT 10
US-09-681-442-72 ; Sequence 72, Application US/09681442
 ; PATENT NO. US20020081634A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Bleirkowski, Michael J.
 ; APPLICANT: Heiriksson, Robert L.
 ; APPLICANT: Paredi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
 ; FILE REFERENCE: 28341/6280FG
 ; CURRENT APPLICATION NUMBER: US/09/681,442
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 09/416,301
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594

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; COUNTRY: USA
; ZEP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/149,718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,487
; APPLICATION NUMBER: 08/480,653
; APPLICATION NUMBER: 08/480,653
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: ANS101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-149-718-10

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Query Match          40.0%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1 AEFR 4
    ||| Db   2 AEFR 5

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RESULT 13
US-09-795-903A-4
; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604 608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO: 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-795-903A-5

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Query Match          40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1 AEFR 4
    ||| Db   7 AEFR 10

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RESULT 15
US-09-794-927-63
; Sequence 63, Application US/09794927
; Patent No. US2001016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 2834/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR APPLICATION NUMBER: 09/416,901
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4

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; PRIORITY FILING DATE: 1999-09-23
; PRIORITY APPLICATION NUMBER: PCT/US99/20881
; PRIORITY FILING DATE: 1999-09-23
; PRIORITY APPLICATION NUMBER: 60/101,594
; PRIORITY FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-794-927-63

Query Match          40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches   4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 AEFR 4
          |||_
Db      7 AEFR 10

Search completed: April 21, 2003, 12:13:36
Job time : 11.3333 secs
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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:08:35 ; Search time 10 Seconds
 (without alignments)
 29.423 Million cell updates/sec

Title: US-09-580-018-10
 Perfect score: 10
 Sequence: 1 AEFRHDGYE 10

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0
 Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database :	Issued_Patents_AA: 1: /cgns2_6/potodata/1/iaa/5A_COMBO.pep: 2: /cgns2_6/potodata/1/iaa/5B_COMBO.pep: 3: /cgns2_6/potodata/1/iaa/6A_COMBO.pep: 4: /cgns2_6/potodata/1/iaa/6B_COMBO.pep: 5: /cgns2_6/potodata/1/iaa/PCTUS_COMBO.pep: 6: /cgns2_6/potodata/1/iaa/backfiles_COMBO.pep: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES		
Result No.	Score	Query Match Length DB ID	Description
1	9	90.0 10 1 US-09-371-930-12	Sequence 12, Appl
2	9	90.0 10 5 PCT-US9401712-12	Sequence 12, Appl
3	5	50.0 5 4 US-08-617-267C-36	Sequence 36, Appl
4	4	40.0 6 1 US-07-843-049A-8	Sequence 8, Appl
5	4	40.0 6 2 US-08-218-97-8	Sequence 8, Appl
6	4	40.0 7 3 US-08-303-061-3	Sequence 3, Appl
7	4	40.0 7 4 US-09-173-941-82	Sequence 82, Appl
8	4	40.0 9 6 5177197-3	Patent No. 5177197
9	4	40.0 10 1 US-07-766-351-1	Sequence 1, Appl
10	4	40.0 10 1 US-08-059-032-1	Sequence 1, Appl
11	4	40.0 10 2 US-08-764-640-11-9	Sequence 119, App
12	4	40.0 10 2 US-08-659-084A-19	Sequence 19, Appl
13	4	40.0 10 3 US-08-973-225-11-9	Sequence 119, App
14	4	40.0 10 3 US-09-244-298A-11-9	Sequence 119, App
15	4	40.0 10 4 US-08-480-332-9	Sequence 9, Appl
16	4	40.0 10 4 US-08-660-531-19	Sequence 19, Appl
17	4	40.0 10 4 US-09-516-704-11-9	Sequence 119, App
18	4	40.0 10 4 US-09-548-312D-63	Sequence 63, Appl
19	4	40.0 10 4 US-09-548-372D-64	Sequence 64, Appl
20	4	40.0 10 4 US-09-548-367D-63	Sequence 63, Appl
21	4	40.0 10 4 US-09-548-367D-64	Sequence 64, Appl
22	4	40.0 10 4 US-09-549-090-11-9	Sequence 119, App
23	4	40.0 10 5 PCT-US91-07290-1	Sequence 1, Appl
24	3	30.0 4 1 US-07-750-330-3	Sequence 3, Appl
25	3	30.0 4 1 US-07-750-330-4	Sequence 4, Appl
26	3	30.0 4 1 US-07-780-790A-9	Sequence 9, Appl
27	3	30.0 4 1 US-08-022-411-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
 US-08-371-930-12
 ; Sequence 12, Application US/08371930
 ; GENERAL INFORMATION:
 ; APPLICANT: Nishimoto, Ikuo
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/371,930
 ; FILING DATE:
 ; CLASSIFICATION: 436
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/019,208
 ; FILING DATE: February 18, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 512-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 20154
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-371-930-12
 Query Match Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRHDGY 9
 11111111
 Db 2 AEFRHDGY 10

RESULT 2 PCT-US94-01712-12

; Sequence 12, Application PC/TUS9401712

; GENERAL INFORMATION:

; APPLICANT: Nishimoto, Ikuo

; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 502 or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01712

FILING DATE:

PRIORITY APPLICATION NUMBER: 08/019,208

FILING DATE: February 18, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/154001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

SEQUENCE CHARACTERISTICS:

LENGTH: 10

TYPE: amino acid

STRANDEDNESS: linear

TOPOLOGY: linear

PCT-US94-01712-12

SEQUENCE FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 10

TYPE: amino acid

STRANDEDNESS: linear

TOPOLOGY: linear

Query Match 90.0%; Score 9; DB 5; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

Qy 1 AEFRHDSGY 9

Db 2 AEFRHDSGY 10

RESULT 3 US-08-617-267C-36

; Sequence 36, Application US/08617267C

; Patent No. 6319498

; GENERAL INFORMATION:

; APPLICANT: Fideis, Mark A. et al

; TITLE OF INVENTION: Modulators of Amyloid Aggregation

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/617,267C

FILING DATE: 14-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/404,831

FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/475,579

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/548,998

FILING DATE: 27-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Deconti, Giulio A.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: PPI-002CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-617-267C-36

RESULT 4 US-07-843-949A-8

Query Match 50.0%; Score 5; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

Qy 5 HDSGY 9

Db 1 HDSGY 5

RESULT 4 US-07-843-949A-8

Sequence 8, Application US/07843949A

PATENT NO. 534935

GENERAL INFORMATION:

APPLICANT: Anderson, Paul J.

APPLICANT: Streuli, Michel

APPLICANT: Schlossman, Stuart F.

TITLE OF INVENTION: DNAs ENCODING PROTEINS ACTIVE IN LYMPHOCYTE-MEDIATED CYTOTOXICITY

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/843,949A

FILING DATE: 19920219

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/460,678

FILING DATE: January 5, 1990

APPLICATION NUMBER: 07/726,607

FILING DATE: July 10, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 00530/021003

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 8:
 LENGTH: 6
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear

Query Match Score 4; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SGYE 10
 Db 1 SGYE 4

RESULT 5
 US-08-218-978-8
 Sequence 8, Application US/08218978
 ; Patent No. 5837811
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Paul J.
 ; APPLICANT: Streuli, Michel
 ; APPLICANT: Schlossman, Stuart F.
 ; TITLE OF INVENTION: DNAs ENCODING PROTEINS ACTIVE IN
 ; TITLE OF INVENTION: LYMPHOCYTE-MEDIATED CYTOTOXICITY
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50z or 5SX
 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 SOFTWARE: WordPerfect (Version 5.0)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/218,978
 FILING DATE: 03/04/2000
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/843,949
 FILING DATE: February 19, 1992
 APPLICATION NUMBER: 07/450,678
 FILING DATE: January 5, 1990
 APPLICATION NUMBER: 07/728,607
 FILING DATE: July 10, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFILE NUMBER: 00530/021003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX: (617) 542-8906
 INFORMATION FOR SEQ ID NO: 8:
 LENGTH: 6
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear

Query Match Score 4; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Length 6;

Qy 7 SGYE 10
 Db 1 SGYE 4

RESULT 6
 US-08-303-861-3
 Sequence 3, Application US/08303861
 ; Patent No. 6086902
 ; GENERAL INFORMATION:
 ; APPLICANT: ZAMB, TIMOTHY
 ; APPLICANT: LIANG, XIAOFENG
 ; APPLICANT: BABIUK, LORNE A.
 ; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
 ; TITLE OF INVENTION: VACCINES
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.1., Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/303,861
 FILING DATE: 09-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARK, FREDDIE K.
 ; REGISTRATION NUMBER: 35,636
 ; REFERENCE/DOCKET NUMBER: 29310-200020.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

Query Match Score 4; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DSGY 9
 Db 2 DSGY 5

RESULT 7
 US-09-173-941-82
 Sequence 8, Application US/09173941
 ; Patent No. 6140081
 ; GENERAL INFORMATION:
 ; APPLICANT: BARBAS, Carlos F.
 ; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
 ; FILE REFERENCE: NOV0815
 ; CURRENT APPLICATION NUMBER: US/09/173,941
 ; CURRENT FILING DATE: 1998-10-16
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 82
 ; LENGTH: 7

; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
 ; OTHER INFORMATION: codon binding sequence
 ; US-09-173-941-B2
 Qy Query Match 40.0%; Score 4; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches+ 0; Indels 0; Gaps 0;
 ;
 4 RHDS 7
 | | |
 Db 1 RHDS 4
 ;
 RESULT 8
 ; Patent No. 5177197
 ; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
 ; FERNSLEDT, CHRISTER; HEIJLAM, ULF; MIYAZONO, KOHEI; CLAESSEN-WELSH,
 ; LENA; HELLDIN, CARL-HENRIK
 ; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
 ; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
 ; NUMBER OF SEQUENCES: 53
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/487,343
 ; FILING DATE: 27-FEB-1990
 ; SEQ ID NO:3;
 ; LENGTH: 9
 ; 5177197-3
 Query Match 40.0%; Score 4; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches+ 0; Indels 0; Gaps 0;
 ;
 RESULT 10
 ; US-08-059-032-1
 ; Sequence 1, Application US/08059032
 ; Patent No. 5424205
 ; GENERAL INFORMATION:
 ; APPLICANT: Sirna, Sukanto
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Stewart Street Tower,
 ; STREET: Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/059-032
 ; FILING DATE: 19930507
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William E.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15270-10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 1;
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /label= "Xaa4 can be either Gln or Lys"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 5
 OTHER INFORMATION: /label= "Xaa5 can be either Met or Nle"
 US-08-059-032-1

Query Match 40.0%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 65; Indels 0; Gaps 0;

Qy 1 AEFR 4
 ||||
 Db 7 AEFR 10

RESULT 12
 US-08-659-984A-19
 Sequence 19, Application US/08659984A
 Patent No. 5942400
 GENERAL INFORMATION:
 APPLICANT: Anderson, John P.
 APPLICANT: Siniha, Sukanto
 APPLICANT: Jacobson-Croak, Kirsten L.
 TITLE OF INVENTION: Assays for Detecting Beta-Secretase
 TITLE OF INVENTION: Inhibition
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Ctr., 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/659_984A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Heslin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15270-002810US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Region
 LOCATION: one-of-(1)
 OTHER INFORMATION: /note= "N-terminal Ser is acetylated."
 US-08-659-984A-19

Query Match 40.0%; Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 65; Indels 0; Gaps 0;

US-08-659-984A-19

Qy 1 AEFR 4
 ||||
 Db 7 AEFR 10

APPLICANT: Podduturi, Surekha
 ATTINENT: Yin, Qun
 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 TITLE OF INVENTION: RECEPTOR
 NUMBER OF SEQUENCES: 244
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/244,298A
 FILING DATE: 11-DEC-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3281
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 119:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10
 TYPE: amino acids
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-244-298A-119

	Query Match	Score 4;	DB 3;	Length 10;
QY	Best Local Similarity 100.0% ; Matches 4 ; Conservative 0 ; Mismatches 0 ; Indels 0	40.0%	Pred. No. 65;	
Db		1 AEFR 4 1 4 AEFR 7		

RESULT 15
 US-08-480-332-9
 ; Sequence 9, Application US/084800332
 ; Patent No. 6180134
 ; GENERAL INFORMATION:
 ; APPLICANT: Zalipsky, Samuel; Woodle, Martin; Martin, Franco
 ; Barenholz, Yechiel
 ; TITLE OF INVENTION: Enhanced Circulation Effector Composit
 ; TITLE OF INVENTION: Method
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,332
 FILING DATE: 7-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/316,436

; FILING DATE: 29-SEP-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/035,443
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohr, Judy M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5325-0115.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Peptide 9, Fig. 13
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; US-08-480-332-9

Query Match 40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6	DSGY 9
Db	3	DSGY 6

Search completed: April 21, 2003, 12:12:57
Job time : 11 secs



4 protein - protein search, using sw model

run on: April 21, 2003, 12:03:55 ; Search time 28 Seconds
 (without alignments)
 309.071 Million cell updates/sec

Title: US-09-580-018-42

Effect score: 217

Sequence: 1 DAEFRHDSGYEVHHQLVFF. DVGSNKGAIIGLMVGGVIA 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

AC	Q16019;	SEQUENCE FROM N.A.	PRELIMINARY;	PRT;	82 AA.
DT	01-NOV-1996	(TREMBLrel. 01; Created)			
DT	01-NOV-1996	(TREMBLrel. 01; Last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21; Last annotation update)			
DE	Beta amyloid peptide (Fragment).				
GN	BETA APP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9236601; PubMed=8476439;				
RA	Dennman R.B., Rosencwraig R., Miller D.L.; A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor. ";				
RT	Biomed. Biophys. Res. Commun. 192:96-103(1993).				
RL	EMBL: S61380; PDB: AAB26564.; -.				
DR	HSSP; P05067; 1BA4.				
DR	InterPro: IPR01255; Beta-APP.				
DR	Pfam: PF03494; Beta APP; 1.				
FT	NON_TER 1 1				
FT	NON_TER 82 82	8938 MW:	F534AA50E579230A CRC64;		
SQ	SEQUENCE 82 AA;				
Query Match	Best Local Similarity 100.0%;	Score 217;	DB 4;	Length 82;	
Matches	Conservative 100.0%;	Pred. No. 1.9e-22;			
Matches	0;	Mismatches 0;	Indels 0;	Gaps 0;	
RESULT 3					
Q16020	DAEFRHDGSGVEVHQQKLVFFAEDVGNSNKGAIGLMVGGVIA 4.2				
AC	Q16020;	PRELIMINARY;	PRT;	82 AA.	
DT	01-NOV-1996	(TREMBLrel. 01; Created)			
DT	01-NOV-1996	(TREMBLrel. 01; Last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21; Last annotation update)			
DE	Beta amyloid peptide (Fragment).				
GN	BETA APP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9236601; PubMed=8476439;				
RA	Dennman R.B., Rosencwraig R., Miller D.L.; A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor. ";				
RT	Biomed. Biophys. Res. Commun. 192:96-103(1993).				
RL	EMBL: S61383; PDB: AAB26565.; -.				
DR	HSSP; P05067; 1BA4.				
DR	InterPro: IPR01255; Beta-APP.				
DR	Pfam: PF03494; Beta APP; 1.				
FT	NON_TER 1 1				
FT	NON_TER 82 82	8882 MW:	F534AA5AB5D9230A CRC64;		
SQ	SEQUENCE 82 AA;				
Query Match	Best Local Similarity 100.0%;	Score 217;	DB 4;	Length 82;	
Matches	Conservative 100.0%;	Pred. No. 1.9e-22;			
Matches	0;	Mismatches 0;	Indels 0;	Gaps 0;	
RESULT 3					
Q16020	DAEFRHDGSGVEVHQQKLVFFAEDVGNSNKGAIGLMVGGVIA 4.2				
AC	Q16020;	PRELIMINARY;	PRT;	82 AA.	
DT	01-NOV-1996	(TREMBLrel. 01; Created)			
DT	01-NOV-1996	(TREMBLrel. 01; Last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21; Last annotation update)			
DE	Beta amyloid peptide (Fragment).				
GN	BETA APP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9236601; PubMed=8476439;				
RA	Dennman R.B., Rosencwraig R., Miller D.L.; A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor. ";				
RT	Biomed. Biophys. Res. Commun. 192:96-103(1993).				
RL	EMBL: S61383; PDB: AAB26565.; -.				
DR	HSSP; P05067; 1BA4.				
DR	InterPro: IPR01255; Beta-APP.				
DR	Pfam: PF03494; Beta APP; 1.				
FT	NON_TER 1 1				
FT	NON_TER 82 82	8882 MW:	F534AA5AB5D9230A CRC64;		
SQ	SEQUENCE 82 AA;				
Query Match	Best Local Similarity 100.0%;	Score 217;	DB 4;	Length 82;	
Matches	Conservative 100.0%;	Pred. No. 1.9e-22;			
Matches	0;	Mismatches 0;	Indels 0;	Gaps 0;	
RESULT 4					
Q1	DAEFRHDGSGVEVHQQKLVFFAEDVGNSNKGAIGLMVGGVIA 4.2				
Db	DAEFRHDGSGVEVHQQKLVFFAEDVGNSNKGAIGLMVGGVIA 5.9				
RESULT 5					
Q16026	DAEFRHDGSGVEVHQQKLVFFAEDVGNSNKGAIGLMVGGVIA 4.2				
ID	Q16026	PRELIMINARY;	PRT;	534 AA.	
AC	Q16026;				
DT	01-NOV-1998	(TREMBLrel. 08; Created)			
DT	01-NOV-1998	(TREMBLrel. 08; Last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21; Last annotation update)			
DE	Amyloid protein (Beta-amyloid protein) (Fragment).				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.				
OC	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98337885; PubMed=9671674;				
RA	Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W., Milligan C.E.;				
RA	"Increased production of amyloid precursor protein provides a				

RT	Anyloid b-protein precursor.
RL	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
DR	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
HSSP; P05067; 1BA4	Cercopithecoidea; Cercopithecidae;
InterPro; IPR001888; A4_APP,	NCBI_TAXID=541;
Pfam; PF02177; A4_EXTR; 1.	RN
Pfam; PF03494; Beta_APP; 1.	SEQUENCE FROM N.A.
PRINTS; PRO00203; AMYLOIDA4;	TISSUE-CEREBELLUM;
PROSITE; PS00319; A4_EXTRA; 1.	MEDLINE=91273117; PubMed=1905108;
PROSITE; PS00320; A4_INTRA; 1.	RA
NON_TER	Podlinsky M.B., Tolan D.R., Selkoe D.J.;
SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;	"Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease."
Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative 0; Score 217; DB 13; Pred. No. 1.8e-21; Mismatches 0; Indels 0; Gaps 0;	RT
QY 1 DAEFRHDSGYEVHQKLVFFAEDVGNSKGAIIGLMVGVVIA 42	Am. J. Pathol. 138:1423-1435 (1991).
Db 436 DAEFRHDSGYEVHQKLVFFAEDVGNSKGAIIGLMVGVVIA 477	RL
RESULT 6	RL
Q9PVLL PRELIMINARY; PRT; 569 AA.	DR
AC Q9PVLL; 01-MAY-2000 (TREMBLrel. 13, Created)	InterPro; IPR001868; A4_APP.
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	PFAM; PF02177; A4_EXTR; 1.
DE Amyloid protein (Fragment).	PFAM; PF03494; Beta_APP; 1.
GN Gallus gallus (Chicken).	PROSITE; PS00319; A4_EXTRA; UNKNOWN_1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR PROSITE; PS00320; A4_INTRA; UNKNOWN_1.
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallidae;	FT SIGNAL 1 17 POTENTIAL.
NCBI_TAXID=9031;	FT CHAIN 597 636 POTENTIAL.
OX	SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F96D56 CRC64;
[1]RN SEQUENCE FROM N.A.	Query Match Score 217; DB 6; Length 695; Best Local Similarity 100.0%; Pred. No. 2.4e-21; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RC TISSUE-BRAIN;	RT
RA Coulson E.J., Paliga K., Breyreuther K., Masters C.L.; RT "What the evolution of the amyloid protein precursor family tells us about its function.";	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
RT Neurochem. Int. 0:0-0(2000).	DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DR EMBL; AF003041; AAF12698.1; -.	DE Putative amyloid precursor protein.
DR HSSP; P05067; 1BA4.	OS Cavia sp.
InterPro; IPR001868; A4_APP.	OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae.
DR Pfam; PF02177; A4_EXTR; 1.	NCBI_TAXID=10143;
DR Pfam; PF03494; Beta_APP; 1.	RN
DR PRINTS; PRO00203; AMYLOIDA4;	SEQUENCE FROM N.A.
DR SMART; SM00006; A4_EXTRA; 1.	RC TISSUE-BRAIN;
DR PROSITE; PS00319; A4_EXTRA; 1.	MEDLINE=91236426; PubMed=91166031;
DR PROSITE; PS00320; A4_INTRA; 1.	RA Beck M., Mueller D., Bigl V.
FT NON_TER	RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and alternative splicing.";
SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;	RT Biochim. Biophys. Acta 1351:17-21 (1997).
Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative 0; Score 217; DB 13; Pred. No. 1.9e-21; Mismatches 0; Indels 0; Gaps 0;	RT
QY 1 DAEFRHDSGYEVHQKLVFFAEDVGNSKGAIIGLMVGVVIA 42	DR X97631; CAA66230.1; -.
Db 472 DAEFRHDSGYEVHQKLVFFAEDVGNSKGAIIGLMVGVVIA 513	DR HSSP; P05067; 1BA4.
RESULT 7	DR InterPro; IPR001868; A4_APP.
Q95KN7 PRELIMINARY; PRT; 695 AA.	DR PF02177; A4_EXTR; 1.
Q95KN7, 01-DEC-2001 (TREMBLrel. 19, Created)	DR PF03494; Beta_APP; 1.
Q95KN7, 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	DR PRINTS; PRO00203; AMYLOIDA4.
Q95KN7, 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DR SMART; SM00006; A4_EXTRA; 1.
Q95KN7, 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	DR PROSITE; PS00320; A4_INTRA; 1.
Q95KN7, 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;
Query Match Score 217; DB 11; Length 695; Best Local Similarity 100.0%; Pred. No. 2.4e-21; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 217; DB 11; Length 695; Best Local Similarity 100.0%; Pred. No. 2.4e-21; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	597	DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA	638	DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00031; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPT1_KUNITZ_1; 1. DR PROSITE; PS00279; BPT1_KUNITZ_2; 1. KW Serine protease inhibitor.
RESULT 9				SEQUENCE FROM N.A. RA Saras M.; Rodolosse A.; Sorribas V.; RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms." RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR AF289218; AAG00593.1; HSSP; P0567; IBA4. InterPro; IPR001868; A4_APP. InterPro; IPR001255; Beta-APP. PFAM; PF02177; A4_EXTRA; 1. PRINTS; PR00203; AMYLOID4. SMART; SM00006; A4_EXTRA; 1. DR PROSITE; PS00319; Beta-APP; 1. DR SMART; SM00030; A4_INTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. SQ SEQUENCE 695 AA; <u>78565 MW</u> ; F201ED02AEC86D95 CRC64;
Q9DGJ8		PRELIMINARY;	PRT;	695 AA. RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms." RL Submitted (JUL-2001) (TREMBLrel. 16, Created) DE Beta-amyloid precursor protein 695 isoform. OS Gallus gallus (Chicken). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus. OX NCBI_TAXID=9031; RN [1]; RP
				SEQUENCE FROM N.A. RA Saras M.; Rodolosse A.; Sorribas V.; RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms." RL Submitted (JUL-2001) (TREMBLrel. 16, Last sequence update) DE Beta-amyloid precursor protein 695 isoform. OS Gallus gallus (Chicken). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus. OX NCBI_TAXID=9031;
				RESULT 11 Q9TU00 PRELIMINARY; PRT; 770 AA. ID Q9TU00 AC Q9TU00 ORIGIN: DR 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DE Amyloid precursor protein. OS Sus scrofa (Pig). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Mammalia; Etheria; Cetartiodactyla; Suina; Suidae; Sus. OX NCBI_TAXID=9823; RN [1]; RP SEQUENCE FROM N.A. RA Kimura A.; Takahashi T.; RT "Amyloid Precursor Protein 770."; RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. DR AB032550; BAA84580.1; -. HSSP; P05067; IAP. InterPro; IPR001868; A4_APP. InterPro; IPR00223; Kunitz_BPTI. DR Pfam; PF002177; A4_EXTRA; 1. DR Pfam; PF03494; Beta-APP; 1. DR Pfam; PF00014; Kunitz_BPTI; 1. DR PRINTS; PR00203; AMYLOID4A. DR PRINTS; PR00759; BASICPTASE. DR ProDom; PD000222; Kunitz_BPTI; 1. DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00031; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPT1_KUNITZ_1; 1. DR PROSITE; PS05279; BPT1_KUNITZ_2; 1. KW Serine protease inhibitor. SQ SEQUENCE 770 AA; <u>88961 MW</u> ; 5F7A1DCB2BC583E CRC64;
Q9DGJ7		PRELIMINARY;	PRT;	751 AA. RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms." RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR AF289219; AAG00594.1; -. HSSP; P0567; IBA4. InterPro; IPR001868; A4_APP. InterPro; IPR001255; Beta-APP. DR InterPro; IPR00223; Kunitz_BPTI. PFAM; PF02177; A4_EXTRA; 1. PFAM; PF03494; Beta-APP; 1.. PRINTS; PR00014; Kunitz_BPTI; 1.. PRINTS; PR00759; BASICPTASE. PRODom; PD000222; Kunitz_BPTI; 1..
				RESULT 12 Q13778 PRELIMINARY; PRT; 97 AA. ID Q13778 AC Q13778 ORIGIN: DR 01-NOV-1996 (TREMBLrel. 01, Created) DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update) DE Amyloid protein (AD-AP) (Fragment). OS Homo sapiens (Human).

Qy 1 DAEFRHDSGEVHHQKLVFAEDVGSNKGAIIGLMVGGVIA 42
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 595 DSEYRHDATAYEVHHQKLVFAEWSNKGAIIGLMVGGVIA 636
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: April 21, 2003, 12:07:22
Job time : 30 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:01:04 ; search time 11 Seconds
(without alignments)
158.364 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAEFRHDSGYEVHKLYFV.....DGSNKGAIIGLMVGGVVIA 42

Scoring table: BL05UN62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40::*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	217	100.0	57	A4_PIG	Q29023 sus scrofa
2	217	100.0	57	A4_DRSM	Q29149 urus marit
3	217	100.0	58	A4_CANFA	Q28280 canis famil
4	217	100.0	58	A4_RABBIT	Q28748 cryctolagus
5	217	100.0	58	A4_SHEEP	Q28757 ovis aries
6	217	100.0	59	A4_BOVIN	Q28053 bos taurus
7	217	100.0	751	A4_SAISC	Q95241 samiri sci
8	217	100.0	770	A4_HUMAN	P05077 homo sapien
9	198	91.2	770	A4_MOUSE	P12023 mus musculus
10	198	91.2	770	A4 RAT	P08592 ratetus norv
11	62	28.6	755	TRM_AGRFT4	P04029 agrobacteri
12	61	28.1	755	TRN_AGRFT	P25017 agrobacteri
13	57	26.3	327	POLG_PIVCH	P21294 potato virus
14	57	26.3	503	Y226_MCPN	P75462 mycoplasma
15	56.5	26.0	378	SLG1 YEAST	P54867 sachcharomyces
16	55.5	25.6	297	FTR_ARCFU	O28075 archaeoglob
17	55	25.3	488	DHAL_PSESP	P33088 pseudomonas
18	55	25.3	3063	POLG_PYVN	P18247 p. genome po
19	54.5	25.1	967	PDB1_ARATH	P93733 arabidopsis
20	54	24.9	284	POLG_PYYO	P11897 potato virus
21	53.5	24.7	708	YNZB_CAEEL	P45972 canenorhodobius
22	53.5	24.7	971	Y228_BORBU	O51246 borrelia bu
23	52	24.0	611	YCR3_YEAST	P25351 sachcharomyces
24	51	23.5	494	COBO_MFCUT	Q53677 mycobacteri
25	51	23.5	769	ITB2_BOVIN	P32592 bos taurus
26	50.5	23.3	915	PDB2_ARATH	P23078 arabidopsis
27	50	23.0	1437	MENB_HAEIN	P44960 haemophilus
28	50	23.0	1437	MRP5_HUMAN	O15440 homo sapien
29	50	23.0	3579	STAN_DROME	Q9v588 drosophila
30	49.5	22.8	1162	VOL2_IBTM	P12651 avian infec
31	49	22.6	246	TPIIS_CUITA	P30741 culic tarsa
32	49	22.6	322	Y853_RICPR	Q9zca7 rickettsia
33	49	22.6	497	GLYA_CHLPN	P9z631 chlamydia p

ALIGNMENTS

RESULT 1	PRT; 57 AA.			
A4_PIG	STANDARD;			
ID A4_PIG				
AC 029023;				
DT 01-NOV-1997 (Rel. 35, Created)				
DT 01-NOV-1997 (Rel. 35, Last sequence update)				
DT 16-OCT-2001 (Rel. 40, Last annotation update)				
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).				
GN APP.				
OS Sus scrofa (Pig).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sus.				
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX NCBI_TaxID:9823;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC TISSUE=Brain;				
RX MEDLINE=92017079; PubMed=1656157;				
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;				
RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis".				
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).				
CC --> FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).				
CC --> SUBCELLULAR LOCATION: Type I membrane protein.				
CC --> SIMILARITY: BELONGS TO THE APP FAMILY.				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).				
CC EMBL: X561127; CAA30592.1; -				
DR HSSP, P05067; IBA4; InterPro; IPR001864; A4_APP.				
DR InterPro; IPR001255; Beta-APP.				
DR Pfam; PF03494; Beta_APP; 1.				
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.				
DR PROSITE; PS00320; A4_INTRA; PARTIAL.				
KW Glycoprotein; Amyloid; Neuron; Transmembrane.				
CC NON_TER 1 1				
DR HSSP, P05067; IBA4; InterPro; IPR001864; A4_APP.				
DR DR DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).				
DR DR TRANSMEM 34 57 POTENTIAL.				
DR DR NON_TER 57 57 SEQUENCE 57 AA; 6172 MW;				
Query Match 100.0%; Score 217; DB 1; Length 57;				
Best Local Similarity 100.0%; Pred. No. 7.9e-22; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

"Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
 RT Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC EMBL: X56130; CAA39951; -.
 CC HSSP; P0567; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 CC pfam; PF03494; Beta_APP; 1.
 DR PROSITE; PS00320; A4_INTRAA; PARTIAL.
 DR Glycoprotein; Amyloid; Neuron; Transmembrane.
 KW KW BETA-AMYLOID PROTEIN (POTENTIAL).
 FT NON_TER 1 1 EXTRACELLULAR (POTENTIAL).
 FT CHAIN 6 48 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN <1 33 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 34 57 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 DR P05067; 1BA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta_APP; 1.
 DR PROSITE; PS00320; A4_INTRAA; PARTIAL.
 DR Glycoprotein; Amyloid; Neuron; Transmembrane.
 KW KW BETA-AMYLOID PROTEIN (POTENTIAL).
 FT NON_TER 1 1 EXTRACELLULAR (POTENTIAL).
 FT CHAIN 6 48 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN <1 33 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 DR P05067; 1BA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta_APP; 1.
 DR PROSITE; PS00320; A4_INTRAA; PARTIAL.
 DR Glycoprotein; Amyloid; Neuron; Transmembrane.
 FT NON_TER 1 1 EXTRACELLULAR (POTENTIAL).
 FT CHAIN 6 48 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN <1 33 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 DR P05067; 1BA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta_APP; 1.
 DR PROSITE; PS00320; A4_INTRAA; PARTIAL.
 DR Glycoprotein; Amyloid; Neuron; Transmembrane.

Query Match 100.0%; Score 217; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKLFVFAEDVGSNKGAIIGLMGGVVIA 42
 Db 6 DAEFRHDSGYEVHKLFVFAEDVGSNKGAIIGLMGGVVIA 47

RESULT 5

A4_SHEEP STANDARD; PRT; 58 AA.
 ID A4_SHEEP
 AC Q28157;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Ovis aries (Sheep).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bos taurus (Bovine); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bos.
 OC NCBI_TaxID=9440;
 RN RN
 RC TISSUE=Brain;
 RX MEDLINE=9201079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC EMBL: X56124; CAA39589.1;
 CC EMBL: X56126; CAA39591.1;
 DR DR

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 CC EMBL: X56130; CAA39951.1;
 CC HSSP; P0567; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR pfam; PF03494; Beta_APP; 1.
 DR PROSITE; PS00320; A4_INTRAA; PARTIAL.
 DR Glycoprotein; Amyloid; Neuron; Transmembrane.
 KW KW BETA-AMYLOID PROTEIN (POTENTIAL).
 FT NON_TER 1 1 EXTRACELLULAR (POTENTIAL).
 FT CHAIN 6 48 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN <1 33 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 DR P05067; 1BA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta_APP; 1.
 DR PROSITE; PS00320; A4_INTRAA; PARTIAL.
 DR Glycoprotein; Amyloid; Neuron; Transmembrane.

Query Match 100.0%; Score 217; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;
 RESULT 6
 A4_BOVIN STANDARD; PRT; 59 AA.
 ID A4_BOVIN
 AC Q28053;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Bos taurus (Bovine); Metazoa; Chordata; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bos.
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bos.
 OC NCBI_TaxID=9913;
 RN RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=9201079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC EMBL: X56124; CAA39589.1;
 CC EMBL: X56126; CAA39591.1;
 DR DR

DR	HSSP; P05067; 1BA4;	DR	Pfam; PF03494; Beta-APP; 1.	
DR	InterPro; IPR01868; A4_APP.	DR	PRINTS; PRO0203; AMYLOIDAA.	
DR	InterPro; IPR01255; Beta-APP.	DR	PRINTS; PRO0759; BASICPTASE.	
DR	Pfam; PF03494; Beta APP; 1.	DR	PRODom; PD000222; Kunitz_BPTI; 1.	
DR	SMART; SM00006; A4_EXTRA; PARTIAL.	DR	SMART; SM00131; KU; 1.	
DR	PROSITE; PS00319; A4_INTRA; PARTIAL.	DR	PROSITE; PS00319; A4_EXTRA; 1.	
KW	Glycoprotein; Amyloid; Neuron; Transmembrane.	DR	PROSITE; PS00320; A4_INTRA; 1.	
FT	NON_TER 1 1	DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.	
FT	CHAIN 7 49	DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.	
FT	DOMAIN <1 34	KW	Glycoprotein; Amyloid; Neuron; Transmembrane; Alternative splicing;	
FT	TRANSMEM 35 58	KW	Serine protease inhibitor.	
FT	DOMAIN 59 >59	FT	Signal; Serine protease inhibitor.	
FT	NON_TER 59 59	FT	BY SIMILARITY.	
SEQUENCE	59 AA; 6414 MW; F43469D488A2E12D CRC64;	FT	CHAIN 17 18	
Query Match	100.0%; Score: 217; DB 1; Length: 59;	FT	CHAIN 751 A4 PROTEIN.	
Best Local Similarity	100.0%; Pred. No. 8.2e-22;	FT	CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).	
Matches 42;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FT	DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).	
Qy	1 DAEFRHDSGYEVHHQKLVFFAEDVGNSNKGAIIGLMVGGVIA 42	FT	TRANSMEM 681 704 PROTEIN (POTENTIAL).	
Db	7 DAEFRHDSGYEVHHQKLVFFAEDVGNSNKGAIIGLMVGGVIA 48	FT	CYTOSMATIC (POTENTIAL).	
RESULT 7	A4_SAISC	STANDARD; PRT; 751 AA.	FT	BPTI/KUNITZ INHIBITOR.
ID	A4_SAISC	STANDARD; PRT; 751 AA.	FT	CLATHRIN-BINDING (BY SIMILARITY).
AC	095241;	FT	ACT SITE 302 REACTIVE BOND.	
DT	15-DEC-1998 (Rel. 37, Created)	FT	DISULFID 291 341 BY SIMILARITY.	
DT	15-DEC-1998 (Rel. 37, Last sequence update)	FT	DISULFID 300 324 BY SIMILARITY.	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	FT	DISULFID 316 337 BY SIMILARITY.	
DE	Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].	FT	CARBONYD 523 523 N-LINKED (GLCNAC-. . .) (PROBABLE).	
DE	APP.	FT	CARBONYD 523 523 N-LINKED (GLCNAC-. . .) (PROBABLE).	
GN	Saimiri sciureus (Common squirrel monkey).	SQ	SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.	Query Match	100.0%; Score: 217; DB 1; Length: 751;	
OC	NCBI_TaxID=9521;	Best Local Similarity	100.0%; Pred. No. 1.1e-20;	
OX	[1]	Matches 42;	Mismatches 0; Indels 0; Gaps 0;	
RN	SEQUENCE FROM N.A.	DE	Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (BN-II) (APP). (Contains: Beta-amyloid protein (Beta-APP) (A-beta)).	
RP	SEQUENCE FROM N.A.	DE	APP OR A4 OR CVAP OR AD1.	
RC	TISSUE=Liver and Kidney;	GN	Homo sapiens (Human).	
RX	MEDLINE=96108492; PubMed=8532114;	OS	Marmosita; Metacercaria; Chordata; Craniata; Vertebrata; Euteleostomi; OC	
RA	"Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy.";	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
RT	Neurobiol. Aging 16:805-808(1995).	OX	NCBI_TaxID=9606;	
RT	"FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O)."	RN	[1]	
RL	-I- SUBCELLULAR LOCATION: Type I membrane protein, -II- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPP MOIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).	RP	SEQUENCE FROM N.A.	
CC	-I- SIMILARITY: BELONGS TO THE APP FAMILY.	RC	TISSUE-Brain;	
CC	-I- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.	CC	MEDLINE=87144572; PubMed=2881207;	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	RN	
CC	CC	RA	Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Miltzhaup G., Beyreuther K., Mueller-Hill B.;	
CC	CC	RA	"The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor." Nature 325:733-736(1987).	
CC	CC	RA	RN	
CC	CC	RA	SEQUENCE FROM N.A. MEDLINE=8812639; PubMed=2893289;	
CC	CC	RA	RN	
CC	CC	RA	Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;	
CC	CC	RA	RN	
CC	CC	RT	"A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors." Nature 331:525-527(1988).	
CC	CC	RL	RN	
CC	CC	RP	[3]	
CC	CC	RP	SEQUENCE FROM N.A. MEDLINE=89138427; PubMed=2783775;	
CC	CC	RA	RN	
CC	CC	RA	Lemaire H.G., Salbaum J.M., Miltzhaup G., Kang J., Bayne R.M.,	

- RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The Pre4 (65) precursor protein of Alzheimer's disease A4 amyloid
RL is encoded by 15 exons";
RN Nucleic Acids Res. 17:517-522(1989).
[4]
- RP SEQUENCE FROM N.A.
RX MEDLINE=97265807; PubMed=9108164;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Hattori M., Tsukahara F., Furukata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakai Y.,
RA "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus.";
RN [5]
RX SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RA Tazzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Guella J.F., Neve R.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor."
RT mRNA associated with Alzheimer's disease.";
RL Nature 351:1802-1804(1997).
RN [6]
RN SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Kitaguchi N., Takahashi Y., Tokushina Y., Shiojiri S., Ito H.,
RT "Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.";
RT RT
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RN SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RA "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.";
RT RT
RN Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN SEQUENCE OF 507-770 FROM N.A.
RX MEDLINE=88124954; PubMed=893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.";
RT RT
RN Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [9]
RN SEQUENCE OF 672-681.
RX MEDLINE=88035004; PubMed=3312495.
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtelotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition and partial sequence of a 4,200-dalton peptide isolated from cortical microvessels.";
RT RT
RN J. Neurochem. 49:1394-1401(1987).
RN [10]
RN SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE=90236310; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.,
RT "Genomic organization of the human amyloid beta-protein precursor gene.";
RT RT
RN Gene 87:257-263(1990).
RN [11]
RN SEQUENCE OF 1-10 FROM N.A.
RP TISSUE-Liver;
RC SEQCODE 1-10
RX MEDLINE=89016647; PubMed=3140222;
RA Schon F.A., Mita S., Sadloc J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABP) encodes a 95-kDa polypeptide.";
RN [12]
RN SEQUENCE OF 18-50.
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.P.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
- RP IDENTITY OF APP WITH NEXIN-II.;
RX MEDLINE=8384866; PubMed=2506449.
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with the Kunitz domain is protease nexin-II.";
RT RT
RN Nature 341:144-147(1989).
RN [14]
- RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE=9211252; PubMed=169731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.,
RT "Protease specificity of Kunitz inhibitor domain of Alzheimer's disease amyloid protein precursor.";
RT RT
RN Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
- RP COMPLEX WITH G(O).
RX MEDLINE=9188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsuuura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding protein G(O).";
RL Nature 362:75-79(1993).
RN [16]
- RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE=9215582; PubMed=10201399;
RA Rossjohn J., Cappa R., Feil S.C., Henry A., McKinstry W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.;
RT "Crystal structure of the N-terminal, growth factor-like domain of Alzheimer amyloid precursor protein.";
RT RT
RN Nat. Struct. Biol. 6:327-331(1999).
RN [17]
- RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RX MEDLINE=91104913; PubMed=2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of Alzheimer's amyloid beta-protein precursor.";
RT RT
RN Biochemistry 29:10018-10022(1990).
RN [18]
- RP STRUCTURE BY NMR OF 289-344.
RX MEDLINE=92031488; PubMed=1718421;
RA Head S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kamarki M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid precursor protein";
RT RT
RN Biochemistry 30:10467-10478(1991).
RN [19]
- RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=94281210; PubMed=7516706;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Sequential NMR resonance assignment of the amyloid beta peptide (25-35) in the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid precursor protein.";
RT RT
RN Biochemistry 33:7788-7796(1994).
RN [20]
- RP STRUCTURE BY NMR OF 696-706.
RX MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in membrane mimicking environment.";
RT RT
RN Biochemistry 35:16094-16104(1996).
RN [21]
- RP STRUCTURE BY NMR OF 672-711.
RX MEDLINE=983359783; PubMed=9633002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle environment. Is the membrane-spanning domain where we think it is?";
RT RT
RN Biochemistry 37:11064-11077(1998).
RN [22]
- RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=20400066; PubMed=10940222;

RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solutions structures in aqueous SDS micelles of two amyloid beta
 peptide fragments of Abeta(1-28) mutated at the alpha-secretase cleavage
 site.";
 RT J. Struct. Biol. 130:142-152(2000).
 RL [23]
 RN STRUCTURE BY NMR OF 681-706
 MEDLINE=20400065; PubMed=10940221;
 RX Zhang S., Iwata K., Lachermann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.B., Lee J.P.;
 RT "The Alzheimer's peptide adopts a collapsed coil structure in
 water."
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;
 RA Dyrts T., Weidemann A., Multhaup G., Salbaum J.-M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 amyloid A4 precursor of Alzheimer's disease.";
 RT J. Struct. Biol. 130:130-141(2000).
 RN [25]
 Query Match 100.0%; Score 217; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAEFRHDGSWEVHHQKLAFEDVGNSNKGAIIGLMVGGVIA 42
 Db 672 DAEFRHDGSWEVHHQKLFFAEDVGNSNKGAIIGLMVGGVIA 713
 RN [1]

RESULT 9

A4_MOUSE	STANDARD	PRT;	770 AA.
ID A4_MOUSE			
AC P12033;			
DT 01-OCT-1989 (Rel. 12, Created)			
DT 01-DEC-1992 (Rel. 24, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Alzheimer's disease amyloid A4 protein homolog precursor			
DE (Amyloidogenic glycoprotein) (AG).			
GN APP.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TAXID=10090;			
OX			
RN [1]			
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.			
RC STRAIN=BALB/C; TISSUE="Brain";			
RX MEDLINE=92096438; PubMed=1756177;			
RA de Strooper B., van Leuven F., van den Berghe H.;			
RT "The amyloid beta protein precursor or proteinase nexin II from mouse RT is closer related to its human homolog than previously reported." RL Biochim. Biophys. Acta 1129:141-143(1991). RN [2]			
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.			
RC TISSUE=Brain;			
RX MEDLINE=88106489; PubMed=3322280;			
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;			
RT protein precursor.";			
RL Biochim. Biophys. Res. Commun. 149:665-671(1987). RN [3]			
RP REVISIONS.			
RA Yamada T.;			
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.			
[4]			
RP SEQUENCE OF 289-364 FROM N.A.			
RC STRAIN=CD-1; TISSUE=Placenta;			
RX MEDLINE=89345111; PubMed=2569710;			
RA Fukuchi K., Martin G.M., Deeb S.S.;			
RT Sequence of the protease inhibitor domain of the A4 amyloid protein RT precursor of <i>Mus domesticus</i> ";			
RL Nucleic Acids Res. 17:5396-5396(1989). RN [5]			

RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209936; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse."
 RL Gene 112:189-195(1992).
 RN [6]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RX TISSUE=Brain, and Kidney;
 RA MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RT Biochem. Biophys. Res. Commun. 158:906-912(1989).
 RL SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPlicing.
 CC -!- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -!- DOMAIN: THE CLATHRIN BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 BPT1/KUNITZ INHIBITOR DOMAIN.
 CC ---
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 CC or send an email to license@isb-sib.ch).
 CC ---
 DR X59377; ; NOT_ANNOTATED_CD5.
 DR ENBL; M18377; ; AAA37138; 1; .
 DR EMBL; X15210; CAA33280; 1; .
 DR MGI; D10603; BAA01456; 1; .
 DR EMBL; M24397; ; AAA39929; 1; .
 DR PR; A27485; ; A27485.
 DR PR; S04855; ; S04855.
 DR PR; S19727; ; S19727.
 DR HSSP; P05067; ; 1AHP.
 DR MGDB; MGT; 88059; ; APP.
 DR InterPro; IPR001868; ; A4_APP.
 DR InterPro; IPR002223; ; Kunitz_BPTI.
 DR Pfam; PF00014; ; Kunitz_BPTI; 1.
 DR Pfam; PF02177; ; A4_EXTRA; 1.
 DR Pfam; PF03494; ; Beta-APP; 1.
 DR PRINTS; PRO00203; ; AMYLOIDAA.
 DR PRINTS; PRO0759; ; BASICPTASE.
 DR PRODOM; PD000222; ; BPT1_KUNITZ_BPTI; 1.
 DR SMART; SM000131; ; KU; 1.
 DR PROSITE; PS00319; ; A4_EXTRA; 1.
 DR PROSITE; PS000320; ; A4_INTRA; 1.
 DR PROSITE; PS00279; ; BPT1_KUNITZ_2; 1.
 DR PROSITE; PS00280; ; BPT1_KUNITZ_1; 1.
 KW Glycoprotein; Amyloid; Neuron; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT DOMAIN 18 699 HOMOLOG.
 FT TRANSMEM 700 723 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.

FT	DOMAIN	287	345	BPTI/KUNITZ INHIBITOR.
FT	SITE	759	762	CLATHRIN-BINDING (BY SIMILARITY).
FT	DISULFID	291	341	BY SIMILARITY.
FT	DISULFID	300	324	BY SIMILARITY.
FT	DISULFID	316	337	BY SIMILARITY.
FT	CARBOHYD	542	542	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	571	571	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARPPLIC	289	289	E->V (IN ISOFORM APP(695)).
FT	VARPPLIC	290	364	MISSING (IN ISOFORM APP(695)).
FT	VARPPLIC	346	380	MISSING (IN ISOFORM APP(751)).
SQ	SEQUENCE	770	AA:	86752 MW;
				26C50DE0890CAF7A CRC84;
Query Match	91.2%	Score 198;	DB 1;	Length 770;
Best Local Similarity	92.9%	Pred. No. 3.e-18;		
Matches 39;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	DAEPRHDGSEVHQKLIVFAEDVGNSNGKAIGLMLGGVVIA 42		
Db	672	DAEFGHDSSGFEVHQKLIVFAEDVGNSNGKAIGLMLGGVVIA 713		
RESULT 10				
A4_RAT	ID A4_RAT	STANDARD:	PRT:	770 AA.
AC	P08592;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Alzheimer's disease amyloid A4 protein precursor			
DE	(Amyloidogenic glycoprotein) (Ag).			
GN	APP.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE OF 1-289 AND 365-770 FROM N.A.			
RC	TISSUE-Brain;			
RX	MEDLINE-88312583; PubMed=2900758;			
RA	Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,			
RA	Seuberg P.H.,			
RT	"Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";			
RL	EMBO J. 7:1365-1370(1988).			
RN	[2]			
RP	SEQUENCE OF 289-364 FROM N.A.			
RC	TISSUE-Liver;			
RX	MEDLINE-89183625; PubMed=26483331;			
RA	Xang J., Mueller-Hill B.;			
RT	"The sequence of the two extra exons in rat preA4 . . ."			
RL	Nucleic Acids Res. 17:2130-2130(1989).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE APP FAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.			
CC				
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DR	X07648; CAA30488.1;			
DR	X14066; CAA32229.1;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
STRAIN=Ach5	PLASMID=priAch5;			
RC	PRIMID=TR2M_AGR4	STANDARD;	PRT:	755 AA.
AC	P04029;			
DT	23-OCT-1986 (Rel. 02, Created)			
DT	23-OCT-1986 (Rel. 02, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	TRYPTophan tumefaciens (EC 1.13.12.3).			
GN	TMS1.			
OS	Agrobacterium tumefaciens.			
OS	Plasmid pTAch5, and Plasmid pTA6NC.			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Rhizobiaceae; Rhizobium.			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RN	PRIMID=8420794; PubMed=632792;			
RA	Gielen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H., Lemmers M., van Montagu M., Scheel J.;			
RA	"the complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefaciens plasmid pTAch5."			
RL	EMBO J. 3:835-846(1984).			
RN	[2]			
RN	SEQUENCE FROM N.A.			

PLASMID=PTIA6NC; PubMed=6584906; MEDLINE=84170374;

RC RX Klei H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D.,
RA Fuller S., Flores C., Paschon J., Nester E., Gordon M.;
RA RT "Nucleotide sequence of the tms genes of the phIA6NC octopine Ti plasmid: two gene products involved in plant tumorigenesis.";
RT RL Proc. Natl. Acad. Sci. U.S.A. 81:1728-1732(1984).
CC -|- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide + CO(2) + H(2)O.

CC -|- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.

CC -|- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ACH5.

CC -|- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF HYDROXYBENZOATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEKS THAT THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.

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CC -|- DR EMBL: K02544; AAA93550; 1; -.

CC -|- DR InterPro: IPR002937; Amino_oxidase.

CC -|- DR InterPro: IPR000205; NAD_binding.

CC -|- DR InterPro: IPR00624; Glycosidase.

CC -|- DR Pfam: PF01593; Amino_oxidase; 1.

CC -|- DR Pfam: PF02027; R01B_R01C; 1.

CC -|- KW Oxidoreductase; Monoxygenase; Auxin biosynthesis; Crown gall tumor; T-DNA; Plasmid.

CC -|- FT VARIANT 718 719 NR -> IQ (IN PTIA6NC).

CC -|- FT VARIANT 721 721 P -> A (IN PTIA6NC).

CC -|- SQ SEQUENCE 755 AA; 83947 MW; 9FD2B83FE001A4D CRC64;

Query Match Score 62; DB 1; Length 755; Best Local Similarity 41.7%; Pred. No. 2.6; Matches 15; Conservative 6; Mismatches 9; Indels 6; Gaps 1;

CC -|- DR EMBL: S15002; S15002.

CC -|- DR InterPro: IPR002937; Amino_oxidase.

CC -|- DR InterPro: IPR00624; Glycosidase.

CC -|- DR Pfam: PF01593; Amino_oxidase; 1.

CC -|- DR Pfam: PF02027; R01B_R01C; 1.

CC -|- KW T-DNA; Plasmid.

CC -|- SQ SEQUENCE 755 AA; 83972 MW; 6FA63E502343136F CRC64;

Query Match Score 61; DB 1; Length 755; Best Local Similarity 41.7%; Pred. No. 2.6; Matches 15; Conservative 6; Mismatches 9; Indels 6; Gaps 1;

CC -|- DR EMBL: S15002; S15002.

CC -|- DR InterPro: IPR002937; Amino_oxidase.

CC -|- DR InterPro: IPR00624; Glycosidase.

CC -|- DR Pfam: PF01593; Amino_oxidase; 1.

CC -|- DR Pfam: PF02027; R01B_R01C; 1.

CC -|- KW T-DNA; Plasmid.

CC -|- SQ SEQUENCE 755 AA; 83972 MW; 6FA63E502343136F CRC64;

RESULT 13

POLG_PYCH STANDARD PRT; 327 AA.

ID POLG_PYCH AC P21294; DT 01-MAY-1991 (Rel. 18, Created)
ID POLG_PYCH AC P21294; DT 01-MAY-1991 (Rel. 18, Last sequence update)
ID POLG_PYCH AC P21294; DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Genome_polyprotein [Contains: Nuclear inclusion protein B (NI-B) (NIB)]
DE (RNA-directed RNA polymerase) (EC 2.7.7.48); Coat protein (CP)]
DE (fragment).

OS Potato virus Y (strain Chinese isolate) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Polyvirus.

OX NCBI_TaxID=12218;

RP SEQUENCE FROM N.A.
RX MEDLINE=91016851; PubMed=2216735;
RT "cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate)." ;
RT Isolate;" ;
RL Nucleic Acids Res. 18:5554-5554 (1990).

CC -|- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA} (N).

CC -|- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.

CC -|- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

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OM protein - protein search, using sw model.
Run on: April 21, 2003, 12:05:20 ; Search time 18 Seconds
(without alignments)
224,314 Million cell updates/sec

Title: US-09-580-018-42
Perfect score: 217
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....DVGSNKGATIGLMGGVVIA 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs., 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73;*
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	217	100.0	42	2	PN0512	beta-amyloid precursor - sheep (fragment)
2	217	100.0	57	2	E60045	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
3	217	100.0	57	2	F60045	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
4	217	100.0	57	2	G60045	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
5	217	100.0	57	2	D60045	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
6	217	100.0	57	2	A60045	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
7	217	100.0	57	2	B60045	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
8	217	100.0	82	2	P00438	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
9	217	100.0	695	1	A4975	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
10	217	100.0	770	1	QRU04	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
11	198	91.2	695	2	A27485	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
12	198	91.2	695	2	M00530	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
13	198	91.2	747	2	JH0773	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
14	133	61.3	33	2	S23094	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
15	63	29.0	755	2	A1328	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
16	62	28.6	755	1	QQAGTR	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
17	61	28.1	755	1	DAAGTT	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
18	57	26.3	327	2	S11435	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
19	57	26.3	503	2	S73843	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
20	56.5	26.0	378	2	S61922	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
21	55.5	25.6	297	2	G69535	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
22	55.5	25.6	678	2	G71526	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
23	55	25.3	291	2	F95015	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
24	55	25.3	317	2	H78832	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
25	55	25.3	488	2	S27652	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
26	55	25.3	3063	2	JS0166	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
27	54.5	25.1	678	2	C81633	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
28	54.5	25.1	832	2	H84848	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)
29	54	24.9	77	2	C97027	Alzheimer's disease amyloid beta protein precursor - sheep (fragment)

RESULT 3

genome polyprotein Na+/H+ antiporter hypothetical prote conserved hypothetical prote hypothetical prote na+/H+ antiporter hypothetical prote nodulin-like prote polyprotein - putative transporter hypothetical prote 3-methyl-2-oxobutyl hypothetical prote signal transduction conserved hypothetical conserved hypothetical

ALIGNMENTS

RESULT 1
PN0512
beta-amyloid protein - guinea pig (fragment)
C; Species: Cavia porcellus (guinea pig)
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C; Accession: PN0512
R; Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohnchi, H.; Res. Commun. 193, 624-630, 1993
A; Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment
A; Reference number: PN0512; MUID:93290653; PMID:7685598
A; Accession: PN0512
A; Residues: 1-42 <S>H>
C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteins
C; Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 7 5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42

RESULT 2
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C; Species: Ovis sp. (sheep)
C; Accession: E60045
C; Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
R; Johnston, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.; Brain Res. Mol. Brain Res. 10, 299-305, 1991
A; Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in a mouse brain
A; Reference number: A60045; MUID:92017079; PMID:1656157
A; Accession: E60045
A; Molecule type: mRNA
A; Residues: 1-57 <J>OH>
A; Cross-references: FMBL:X56130
C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteins
C; Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 217; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42

F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
 C;Species: Sus scrota domestica (domestic pig)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
 A;Reference number: A60045; PMID:1656157
 A;Accession: F60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56127; NID:91895; PID:CAA39592;1; PMID:91896
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match	100.0%	Score: 217;	DB 2;	Length: 57;	
Best Local Similarity	100.0%	Pred. No. 1e-21;			
Matches	42;	Conservative 0;	Indels 0;	Gaps 0;	

Qy 1 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 6 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 47

RESULT 4
 G60045 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
 C;Species: Cavia porcellus (guinea pig)
 C;Accession: G50045
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
 A;Reference number: A60045; PMID:92017079; PMID:1656157
 A;Accession: G60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56126
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match	100.0%	Score: 217;	DB 2;	Length: 57;	
Best Local Similarity	100.0%	Pred. No. 1e-21;			
Matches	42;	Conservative 0;	Indels 0;	Gaps 0;	

Qy 1 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 6 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 47

RESULT 5
 D60045 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Accession: D60045
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
 A;Reference number: A60045; PMID:92017079; PMID:1656157
 A;Accession: D60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56124
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match	100.0%	Score: 217;	DB 2;	Length: 57;	
Best Local Similarity	100.0%	Pred. No. 1e-21;			
Matches	42;	Conservative 0;	Indels 0;	Gaps 0;	

Qy 1 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42

Db 6 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 47

RESULT 6
 A60045 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
 C;Species: Canis lupus familiaris (dog)
 C;Accession: A60045
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A;Reference number: A60045; PMID:92017079; PMID:1656157
 A;Accession: A60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56125
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match	100.0%	Score: 217;	DB 2;	Length: 57;	
Best Local Similarity	100.0%	Pred. No. 1e-21;			
Matches	42;	Conservative 0;	Indels 0;	Gaps 0;	

Qy 1 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 6 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 47

RESULT 7
 B60045 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C;Species: Ursus maritimus (polar bear)
 C;Accession: B60045
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A;Reference number: A60045; PMID:92017079; PMID:1656157
 A;Accession: B60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56128; NID:92165; PID:CAA39593;1; PMID:92166
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match	100.0%	Score: 217;	DB 2;	Length: 57;	
Best Local Similarity	100.0%	Pred. No. 1e-21;			
Matches	42;	Conservative 0;	Indels 0;	Gaps 0;	

Qy 1 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 6 DAEFRHDSGEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 47

RESULT 8
 P00438 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Accession: P00438; C60045
 C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
 A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
 A;Reference number: P00438; PMID:1445331
 A;Accession: P00438
 A;Molecule type: DNA
 A;Residues: 1-82 <DAV>
 A;Cross-references: GB:M83558; GB:M83657
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A; Reference number: A60045; MUID:92017079; PMID:1656157

A; Molecule type: mRNA

A; Residues: 12-68 <JOH>

C; Cross-references: EMBL:X56129

C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase C; Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match Score 217; DB 2; Length 82;

Best Local Similarity 10.0%; Pred. No. 1.6e-21;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9

A49795 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C; Species: Macaca fascicularis (crab-eating macaque)

C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C; Accession: A49795

R; Podlinsky, M.B.; Tolani, D.R.; Selkoe, D.J.

An. J. Pathol. 138, 1423-1435, 1991

A; Title: Homology of the amyloid beta protein precursor in monkey and human supports a P

A; Reference number: A49795; MUID:91273117; PMID:1105108

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-695 <POD>

C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase C; Keywords: alternative splicing

Query Match Score 217; DB 1; Length 695;

Best Local Similarity 10.0%; Pred. No. 1.6e-20;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10

A49795 Alzheimer's disease amyloid beta protein precursor [validated] - human coagulation factor Xa inhibitor

N; Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular

protein precursor splice form APP(770)

C; Species: Homo sapiens (man)

C; Date: 30-Jun-1998 #sequence 28-Jul-1995 #text_change 15-Sep-2000

C; Accession: S02260; S05194; A32277; A33260; A33486; I39452; I39453; I59562; A44

4668; A28583; A29302; A60805; JI0038; S06121; A63555; A59011; A38384; S29076; S38525; S3

R; Lemaire, H.G.; Salbaum, J.M.; Muirhead, G.; Bayne, R.M.; Unterbeck, A.; Bey

A; Title: The PreA(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by

A; Reference number: S02260; MUID:89128427; PMID:2783775

A; Molecule type: DNA

A; Residues: 1-288, 'V', 365-770 <LEM1>

A; Cross-references: EMBL:XI1366

A; Note: alternative splice form APP(695)

R; Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A; Reference number: S05194

A; Accession: S05194

A; Molecule type: DNA

A; Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>

A; Cross-references: EMBL:XI1366; NID:35598; PIDN:CAA31830.1; PMID:9871360

A; Note: alternative splice form APP(695)

R; La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A; Molecule type: DNA

A; Residues: 687-692, 'G', 694-718 <KAM1>

A; Cross-references: GB:S4135; NID:9257377; PIDN:ABA23645.1; PMID:9257378

A; Experimental source: familial Alzheimer disease family SB

A; Note: sequence extracted from NCBI backbone (NCBIP:115374)

A; Accession: B44017

A; Molecule type: DNA

A; Residues: 693-698, 'P', 705-737 <MUR>

A; Cross-references: GB:S57665; NID:9236720; PIDN:AAB19991.1; PMID:9236721

R; Kamino, K.; Orr, H.T.; Payami, H.; Wijisman, B.M.; Alonso, S.M.; Puist, S.M.; Anders

arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart

Am. J. Hum. Genet. 51, 998-1014, 1992

A; Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

A; Reference number: A44017; MUID:1415269

A; Molecule type: DNA

A; Residues: 687-692, 'G', 694-718 <KAM1>

A; Cross-references: GB:S4135; NID:9257377; PIDN:ABA23645.1; PMID:9257378

A; Experimental source: familial Alzheimer disease family SB

A; Note: sequence extracted from NCBI backbone (NCBIP:115374)

A; Molecule type: DNA

A; Residues: 693-698, 'P', 705-737 <MUR>

A; Cross-references: GB:S4135; NID:9257377; PIDN:ABA23645.1; PMID:9257378

A; Experimental source: familial Alzheimer disease family SB

A; Note: sequence extracted from NCBI backbone (NCBIP:115374)

A; Molecule type: DNA

A;Cross-references: GB:D10603; NID:920328; PIDN:BA01456..1; PID:9220329	
C;Genetics:	
C;Map: Position: 16C3	
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protease inhibitor	
C;Keywords: alternative splicing; amyloid; transmembrane protein	
Query Match 91.2%; Score 198; DB 2; Length 695;	
Best Local Similarity 92.9%; Pred. No. 5.1e-18;	
Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
Qy 1 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMVGGVVIA 42	
Db 597 DAEFHDGSGFEVRHQKLVFFAEDVGSNKGATIGLMVGGVVIA 638	
RESULT 12	
S00550	Alzheimer's disease amyloid beta protein precursor - rat
N;Alternative names: beta A4 amyloid protein	
C;Species: Rattus norvegicus (Norway rat)	
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999	
C;Accession: S00550; A41245; A39820; S46251	
R;Shivers, B.D.; Hilbun, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seuburg, P.H.	
EMBO J. 7, 1365-1370, 1988	
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain	
A;Reference number: S00550; MUID:88312583; PMID:2900758	
A;Accession: S00550	
A;Molecule type: mRNA	
A;Residues: 1-95</SH1>	
A;Cross references: EMBL:X07648; NID:955616; PIDN:CAA30488..1; PID:955617	
R;Schubert, D.; Schroeder, R.; Lacorbiere, M.; Saiton, T.; Cole, G.	
Science 241, 222-226, 1988	
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core.	
A;Reference number: A41245; MUID:88264430; PMID:2968652	
A;Accession: A41245	
A;Molecule type: protein	
A;Residues: 18-37, X, 39-40, 'X', 42-44 <SCH>	
A;Note: evidence for heparan sulfate attachment	
R;Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.	
FEBS Lett. 319, 109-116, 1994	
A;Title: The beta-A4 amyloid precursor protein binding to copper.	
A;Reference number: S46251; MUID:4320527; PMID:7913895	
A;Contents: annotation; copper binding sites	
A;Note: rat peptides were isolated but not sequenced	
R;Potempaska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.	
J. Biol. Chem. 266, 8464-8469, 1991	
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain	
A;Reference number: A39820; MUID:9121087; PMID:1673681	
A;Accession: A39820	
A;Status: preliminary	
A;Molecule type: protein	
A;Residues: 18-32 <PON>	
A;Experimental source: brain	
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type protease inhibitor	
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protease inhibitor	
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein	
F;625-648/Domain: transmembrane #status predicted <TM>	
Query Match 91.2%; Score 198; DB 2; Length 695;	
Best Local Similarity 92.9%; Pred. No. 5.1e-18;	
Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
Qy 1 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMVGGVVIA 42	
Db 597 DAEFHDGSGFEVRHQKLVFFAEDVGSNKGATIGLMVGGVVIA 638	
RESULT 13	
JH073	Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)	
C;Accession: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999	
C;Accession: JH073	

R, Okado, H.; Okamoto, H., Biochim. Biophys. Res. Commun. 189, 1561-1568, 1992 A; Title: A Xenopus homologue of the human beta-amyloid precursor protein: development A; Reference number: JH0773; MUID:128205 A; Accession: JH0773 A; Molecule type: mRNA A; Residues: 1-747 <OKA> A; Cross-references: GB:S52417; NID:9263150; PID:AAB24853.1; PID:g263151 A; Experimental source: larva C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteins C; Keywords: alternative splicing; amyloid fibril; domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Matches 16; Conservative 5; Mismatches 9; Indels 6; Gaps 1;
Qy 7 DSGEVHHRQLVFFAEDVGSNKGAIIIGIMVGIVIA 42
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Db 223 DSG-----RIGFFPEDVPKPVAIIGACISGLVVA 252

Search completed: April 21, 2003, 12:07:46
Job time : 20 secs

GenCore version 5.1.4.p5 4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:06:50 ; Search time 15 Seconds

(without alignments)
211.719 Million cell updates/sec

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAEFRHDSGYEVHQKLVFF.....DVGSNKGAIIGLMVGGVVIA 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 28829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA: *
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NNEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	217	10.0	42 8 US-09-923-055-2	Sequence 2, Appli
2	217	10.0	42 9 US-10-051-496-2	Sequence 2, Appli
3	217	10.0	42 9 US-10-082-804-7	Sequence 7, Appli
4	217	10.0	42 9 US-09-962-174	Sequence 37, Appli
5	217	10.0	42 9 US-09-848-616-174	Sequence 37, Appli
6	217	10.0	42 9 US-09-865-294-65	Sequence 65, Appli
7	217	10.0	42 10 US-09-867-847-1	Sequence 1, Appli
8	217	10.0	42 10 US-09-956-625-26	Sequence 26, Appli
9	217	10.0	42 10 US-09-731-460-1	Sequence 1, Appli
10	217	10.0	43 9 US-10-076-708-7	Sequence 7, Appli
11	217	10.0	43 9 US-10-051-496-1	Sequence 1, Appli
12	217	10.0	43 9 US-10-217-559-1	Sequence 1, Appli
13	217	10.0	43 10 US-09-966-1	Sequence 1, Appli
14	217	10.0	43 10 US-09-904-987-1	Sequence 1, Appli
15	217	10.0	43 10 US-09-808-037-3	Sequence 3, Appli
16	217	10.0	43 10 US-09-866-112-3	Sequence 3, Appli
17	217	10.0	43 10 US-09-972-475-1	Sequence 1, Appli
18	217	10.0	43 10 US-09-992-800-1	Sequence 1, Appli
19	217	10.0	43 10 US-09-895-443-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1	Sequence 2, Application US/08923055
	Patent No. US20010016327A1
	GENERAL INFORMATION:
	APPLICANT: Dana Giulian
	TITLE OF INVENTION: Identification of Agents that Protect Against Inflammatory Injury to Neurons
	NUMBER OF SEQUENCES: 2
	CORRESPONDENCE ADDRESS:
	ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
	ADDRESS: 5 No. US2010016327A1rsls LLP
	STREET: One Liberty Place - 46th Floor
	CITY: Philadelphia
	STATE: PA
	ZIP: 19103
	COMPUTER READABLE FORM:
	COMPUTER: IBM PS/2
	OPERATING SYSTEM: PC-DOS
	SOFTWARE: WORDPERFECT FOR WINDOWS 6.0
	CURRENT APPLICATION DATA:
	APPLICATION NUMBER: US/08/923,055
	FILING DATE: Sept-03-97
	CLASSIFICATION: 435
	PRIOR APPLICATION DATA:
	APPLICATION NUMBER:
	FILING DATE:
	ATTORNEY/AGENT INFORMATION:
	NAME: Lori Y. Beardell
	REGISTRATION NUMBER: 34,293
	TELECOMMUNICATION INFORMATION:
	TELEPHONE: (215) 568-3100
	TELEFAX: (215) 568-3439
	INFORMATION FOR SEQ ID NO: 2:
	SEQUENCE CHARACTERISTICS:
	LENGTH: 42 amino acids
	TYPE: amino acid
	TOPOLOGY: linear
	MOLECULE TYPE: peptide

US-08-923-055-2 Best Local Similarity 100.0%; Pred. No. 1.5e-22; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVEFAEDVGSNKGATIGLMGVVIA 4.2
Db 1 DAEFRHDSGYEVHQKLVEFAEDVGSNKGATIGLMGVVIA 4.2

RESULT 3
US-10-082-804-7 Application US/10082804
; Sequence 7, Application US/10082804
; Publication No. US20020194632A1
GENERAL INFORMATION:
; APPLICANT: Kei-Lai L. Fong
; TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-39) and Abeta(1-42) and Abeta (1-43)

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kei-Lai L. Fong
; STREET: 1004 West 8th Avenue
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.44MB storage
COMPUTER: IBM PC Compatibles
OPERATING SYSTEM: Windows
SOFTWARE: MS No. US20020182660A1epad

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,496
FILING DATE: 18-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/784,854A
FILING DATE: 16-Feb-2001
APPLICATION NUMBER: 60/183,407
FILING DATE: 18-February-2000

ATTORNEY/AGENT INFORMATION:
NAME: Koenig, C. Frederick III
REGISTRATION NUMBER: 29,662
REFERENCE/DOCKET NUMBER: FBI-PT001.1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-6400
TELEFAX: (215) 568-6499

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 Amino Acid
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein

FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1-42
IDENTIFICATION METHOD: Similarity to other sequences, hydro-phobic
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1-42
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-051-496-2

Query Match 100.0%; Score 217; DB 9; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.5e-22; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVEFAEDVGSNKGATIGLMGVVIA 4.2
Db 1 DAEFRHDSGYEVHQKLVEFAEDVGSNKGATIGLMGVVIA 4.2

RESULT 3
US-10-082-804-7 Application US/10082804
; Sequence 7, Application US/10082804
; Publication No. US20020194632A1
GENERAL INFORMATION:
; APPLICANT: McCollough, Lisa E.
; TITLE OF INVENTION: Transgenic Knockouts of BACE-1
; FILE REFERENCE: MBHB 02-329-A
; CURRENT APPLICATION NUMBER: US/10/082,804
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/271,092
; PRIOR FILING DATE: 2001-02-23
; PRIORITY NUMBER: 60/271,514
; PRIORITY FILING DATE: 2001-02-26
; PRIORITY APPLICATION NUMBER: 60/293,762
; PRIORITY FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 7
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: A-beta 42 sequence.
US-10-082-804-7 Application US/10082804
Query Match 100.0%; Score 217; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-22; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVEFAEDVGSNKGATIGLMGVVIA 4.2
Db 1 DAEFRHDSGYEVHQKLVEFAEDVGSNKGATIGLMGVVIA 4.2

RESULT 4
US-09-962-955C-37 Application US/09962955C
; Sequence 37, Application US/09962955C
; Publication No. US20030013648A1
GENERAL INFORMATION:
; APPLICANT: Gerardo M. Castillo
; APPLICANT: Alan D. Show
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrick M. Dwyer
; STREET: ProteoTech, Inc., 1818 Westlake Avenue N, Suite 114
; CITY: Seattle
; STATE: WA (Washington)
; COUNTRY: United States of America
; ZIP: 98109
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Wordperfect 9
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,955C
; FILING DATE: 22-August-2001
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/938,275
; FILING DATE: 22-August-2001
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

Query Match 100.0%; Score 217; DB 10; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.5e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 9
 US-09-731-460-1

; Sequence 1, Application US/09731460
 ; Patent No. US20020137112A1

; APPLICANT: Chojier, Mario

; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
 Disease

; FILE REFERENCE: CHOJIER-04302

; CURRENT APPLICATION NUMBER: US/09/731,460

; CURRENT FILING DATE: 2000-12-07

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 42

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

Query Match 100.0%; Score 217; DB 10; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.5e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 10
 US-10-076-708-7

; Sequence 7, Application US/10076708
 ; Patent No. US20020164657A1

; GENERAL INFORMATION:

; APPLICANT: Sharma, Satish

; TITLE OF INVENTION: Assays for Accessing Aa-Tau Aggregation

; FILE REFERENCE: 6322

; CURRENT APPLICATION NUMBER: US/10/076,708

; CURRENT FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 43

; TYPE: PRT

; ORGANISM: Homo sapiens

; SEQ ID NO: 7

Query Match 100.0%; Score 217; DB 9; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 11
 US-10-051-496-1
 ; Sequence 1, Application US/10051496
 ; Publication No. US20020182660A1
 ; GENERAL INFORMATION:

APPLICANT: Kei-Lai L. Fong

TITLE OF INVENTION: N- and C-Terminus Specific Immunoassays for Full Length Beta-Amyloid Peptide - Abeta(1-40), Abeta(1-41), Abeta(1-43)

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADRESSEEE: Kei-Lai L. Fong
 STREET: 1004 West 8th Avenue

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.50 inch, 1.44MB storage

COMPUTER: IBM PC Compatibles

OPERATING SYSTEM: Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/051,496

FILING DATE: 18-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/784,854A

FILING DATE: 16-Feb-2001

APPLICATION NUMBER: 60/183,407

FILING DATE: 18-February-2000

ATTORNEY/AGENT INFORMATION:

NAME: Koenig, C. Frederick III

REGISTRATION NUMBER: 29,662

REFERENCE/DOCKET NUMBER: PBI-PT001.1

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INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

INDIVIDUAL ISOLATE: <Unknown>

ORGANISM: <Unknown>

CELL TYPE: <Unknown>

IMMEDIATE SOURCE:

LITERARY: <Unknown>

CLONE: <Unknown>

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

RELEVANT RESIDUES IN SEQ ID NO: 1:FROM 1 TO 43

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-051-496-1

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 217; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-22;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Publication No. US20030069445A1
; GENERAL INFORMATION:
; APPLICANT: AUDIA, James
; APPLICANT: HYSLOP, Paul
; APPLICANT: NIJSSEN, Jeffrey
; APPLICANT: THOMPSON, Richard
; APPLICANT: TUNG, Jay
; APPLICANT: TANNER, Laura
; TITLE OF INVENTION: BIOLOGICAL REAGENTS AND METHODS FOR DETERMINING THE
; TITLE OF INVENTION: MECHANISM IN THE GENERATION OF BETA-AMYLOID PEPTIDE
; CURRENT APPLICATION NUMBER: US/10/217,459
; CURRENT FILING DATE: 2002-08-14
; PRIORITY APPLICATION NUMBER: US 09/164,390
; PRIORITY FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: beta-amyloid precursor protein
; US-10-217-459-1

Query Match 100.0%; Score 217; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42

RESULT 13
US-09-280-966-1
; Sequence 1, Application US/09280966
; Patent No. US20010020097A1
; GENERAL INFORMATION:
; APPLICANT: JAMES E. AUDIA
; BEVERLY K. FOLMER
VARGHESE JOHN
JEFFREY S. NISSEN
WARREN J. PORTER
EUGENE D. THORSETT
JING WU

TITLE OF INVENTION: N-(ARYL/HETEROARYLACETYL) AMINO ACID ESTERS, PHARMACEUTICAL COMPOSITIONS COMPRISING SAME, AND METHODS FOR INHIBITING -AMYLOID PEPTIDE RELEASE AND/OR ITS NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280-966
FILING DATE: 30-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,191
FILING DATE: 21 Nov 1997
APPLICATION NUMBER: 60/077,175
FILING DATE: 22 Nov 1996
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113

; REFERENCE/DOCKET NUMBER: 002010-335
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-622-7300
; TELEFAX: 650-622-2459
; INFORMATION FOR SEQ ID NO: 1;
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1;
US-09-280-966-1

Query Match 100.0%; Score 217; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42

RESULT 14
US-09-904-987-1
; Sequence 1, Application US/09904987
; Patent No. US20020037908A1
; GENERAL INFORMATION:
APPLICANT: NO. US20020037908Alactyl, Inc.
TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Pre^f
TITLE OF INVENTION: Protein Assembly or Aggregation
FILE REFERENCE: 42108/26146
CURRENT FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO: 1
LENGTH: 3
TYPE: PRT
ORGANISM: homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI ENTREZ / QRHUA4
DATABASE ENTRY DATE: 2000-09-15
RELEVANT RESIDUES: (672)..(714)
US-09-904-987-1

Query Match 100.0%; Score 217; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLMGGVVIA 42

RESULT 15
US-09-808-037-3
; Sequence 3, Application US/09808037
; Patent No. US2002002311A1
; GENERAL INFORMATION:
APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
FILE REFERENCE: SOLOMON-2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.0
; SEQ_ID NO 3
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-3

Query Match 100 %; Score 217; DB 10; Length 43;
Best Local Similarity 100 %; Pred. No. 1.6e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVIA 42
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42

Search completed: April 21, 2003, 12:08:28
Job time : 15 secs

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:08:10 ; Search time 11.6667 Seconds
(without alignments)
82.401 Million cell updates/sec

Title: US-09-580-018-9
Perfect score: 10
Sequence: 1 DAEFRHDSGY 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : PIR73:
1: pir1:
2: pir2:
3: pir3:
4: Pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	5	2 A26830	mitosis inhibiting peptide - mouse
2	3	30.0	7	2 PT0283	C;Species: Mus musculus (house mouse)
3	3	30.0	2	2 S78036	C;Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
4	3	30.0	9	2 P10139	C;Accession: A26830
5	3	30.0	10	2 A59272	R;Reichelt, K.; Elgjo, K.; Edminson, P.D. Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
6	3	30.0	10	2 PT0243	A;Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
7	3	30.0	10	2 PH090	A;Reference number: A26830; PMID:3619940
8	2	20.0	3	3 PT0571	A;Accession: A26830
9	2	20.0	4	2 S09478	A;Molecule type: protein
10	2	20.0	4	2 PT0633	A;Residues: 1-5 <RET>
11	2	20.0	4	2 PT0711	C;Superfamily: unassigned animal peptides
12	2	20.0	4	2 PT0698	C;Keywords: blocked amino end; pyroglutamic acid (Gln) #status experimental
13	2	20.0	4	2 PT0677	F;1/Modified site: Pyrrolidine carboxylic acid (Gln) #status experimental
14	2	20.0	4	2 PT0706	Query Match 30.0%; Score 3; DB 2; Length 5;
15	2	20.0	4	2 PT0675	Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
16	2	20.0	4	2 PT0566	Query Match 1 DAE 3
17	2	20.0	5	2 C23751	Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
18	2	20.0	5	2 A41225	Query Match 30.0%; Score 3; DB 2; Length 7;
19	2	20.0	5	2 B41225	Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
20	2	20.0	5	2 D66274	Query Match 30.0%; Score 3; DB 2; Length 7;
21	2	20.0	5	2 B37988	Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
22	2	20.0	5	2 A44692	Query Match 1 DAE 3
23	2	20.0	5	2 JTF0520	Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
24	2	20.0	5	2 D44823	Query Match 1 DAE 3
25	2	20.0	5	2 PT0596	Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
26	2	20.0	5	2 PT0513	Query Match 1 DAE 3
27	2	20.0	5	2 PT0600	Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
28	2	20.0	5	2 PT0608	Query Match 1 DAE 3
29	2	20.0	5	2 PT0669	Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 1

A26830
mitosis inhibiting peptide - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C;Accession: A26830
R;Reichelt, K.; Elgjo, K.; Edminson, P.D.
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
A;Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
A;Reference number: A26830; PMID:3619940
A;Accession: A26830
A;Molecule type: protein
A;Residues: 1-5 <RET>
C;Superfamily: unassigned animal peptides
C;Keywords: blocked amino end; pyroglutamic acid (Gln) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Query Match 30.0%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

PT0283
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: PT0283
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
A;Reference number: PT0222; PMID:1899102
A;Accession: PT0283
A;Molecule type: DNA
A;Residues: 1-7 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

S78036 ribosomal protein Yms-B, mitochondrial - yeast (*Saccharomyces cerevisiae*) (fragment)
C;Species: *Saccharomyces cerevisiae*
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C;Accession: S78036
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittmeier, J.; Eur. J. Biochem. 245, 449-56, 1997
A;Title: Identification and characterization of the genes for mitochondrial ribosomal proteins
A;Reference number: S78018; MUID:97296414; PMID:9151978
A;Accession: S78036
A;Molecule type: protein
A;Residues: 1-8 <KID>
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match	30.0%	Score 3;	DB 2;	Length 8;
Best Local Similarity	100.0%	Pred. No. 2.8e+05;	Mismatches 0;	Gaps 0;
Matches 3;	Conservative			
Db	6 DSG 8			

RESULT 4
PJ0139 carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - *Pseudomonas carboxydoflava* (fragment)
C;Species: *Pseudomonas carboxydoflava*
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
R;Kraut, M.; Hugendieck, I.; Hervig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotropes
A;Reference number: PL0138; MUID:90055678; PMID:2818128
A;Molecule type: protein
A;Residues: 1-9 <KID>
A;Note: 2-Met is also found
C;Comment: Cardon-monoxide dehydrogenase consists of three polypeptide chains: large, medium, small
C;Keywords: oxidoreductase

Query Match	30.0%	Score 3;	DB 2;	Length 9;
Best Local Similarity	100.0%	Pred. No. 2.4e+05;	Mismatches 0;	Gaps 0;
Matches 3;	Conservative			
Qy	1 DAE 3			
Db	7 DAE 9			

RESULT 5
A59272 peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain
N;Alternate names: peptide N-glycosidase
C;Species: *Prunus dulcis* var. *sativa* (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C;Accession: A59272
R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Bur. J. Biochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
A;Reference number: A59272; MUID:98181894; PMID:9523720
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ALR>
C;Keywords: hydrolase

Query Match	30.0%	Score 3;	DB 2;	Length 10;
Best Local Similarity	100.0%	Pred. No. 1.4e+03;	Mismatches 0;	Gaps 0;
Matches 3;	Conservative			
Qy	8 SGY 10			
Db	3 SGY 5			

RESULT 6
PR0243 Ig heavy chain CRD3 region (clone 2-103A) - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PR0243
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PR0222; MUID:91108337; PMID:1899102
A;Accession: PR0243
A;Molecule type: DNA
A;Residues: 1-10 <YAN>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 SGY 10
Db 7 SGY 9

RESULT 7
PH0900 T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0900
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbergk, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allelic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0900
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: myelin basic protein-immunized T-cell
C;Keywords: T-cell receptor

Query Match	30.0%	Score 3;	DB 2;	Length 10;
Best Local Similarity	100.0%	Pred. No. 1.4e+03;	Mismatches 0;	Indels 0; Gaps 0;
Matches 3;	Conservative			
Qy	7 DSG 9			
Db	5 DSG 7			

RESULT 8
PR0571 T-cell receptor beta chain V-D-J region (141-10M) - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PR0571
R;Freaney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PR0509; MUID:91277601; PMID:1711558
A;Accession: PR0571
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <PEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match	20.0%	Score 2;	DB 3;	Length 3;
Best Local Similarity	100.0%	Pred. No. 2.8e+05;	Mismatches 0;	Indels 0; Gaps 0;
Matches 2;	Conservative			
Qy	8 SGY 10			
Db	3 SGY 5			

Qy 8 SG 9
 Db 1 |
 Db 2 SG 3

RESULT 9
S09478 globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
 N;Alternate names: IIS globulin alpha subunit gamma chain
 C;Species: Cucurbita sp. (cucurbit)
 C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
 C;Accession: S09478
 R;Ohmura, M.; Hara, I.; Matsubara, H.
 Plant Cell Physiol. 21: 157-167, 1980
 A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and
 A;Reference number: S09066
 A;Accession: S09478
 A;Molecule type: protein
 A;Residues: 1-4 <OHM>

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GY 10		8 SG 9
Db 3 GY 4		2 SG 3

RESULT 10
PT0633 T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0633
 R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; PMID:1711558
 A;Accession: PT0633
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEED>
 A;Experimental source: newborn thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SG 9		8 SG 9
Db 2 SG 3		2 SG 3

RESULT 11
PT0711 T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0607
 R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
 A;Reference number: PT0509; PMID:1711558
 A;Accession: PT0607
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEEL>
 A;Experimental source: newborn thymus, strain BALB/c, 120-2J
 A;Accession: PN0674
 A;Status: translation not shown
 A;Molecule type: DNA

A;Residues: 1-4 <FE2>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
 A;Accession: PT0678
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FE3>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
 A;Accession: PT0570
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FE4>
 A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
 A;Accession: PT0711
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FE5>
 A;Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SG 9		8 SG 9
Db 2 SG 3		2 SG 3

RESULT 12
PT0698 T-cell receptor beta chain V-D-J region (126-1AH) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997
 C;Accession: PT0346; PT0698; PT0583
 R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; PMID:1711558
 A;Accession: PT0546
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 126-1AH
 A;Accession: PT0608
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FE3>
 A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2C
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SG 9		8 SG 9
Db 2 SG 3		2 SG 3

RESULT 13
PT0677 T-cell receptor beta chain V-D-J region (126-1BG) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0558; PT0677
 R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-4 <PPEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c, 126-1BG

A;Accession: PR0677

A;Molecule type: DNA

A;Residues: 1-4 <PE2>

A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1BH

C;Keywords: T-cell receptor

Qy	8	SG	9
I	1		
D	2	SG	3

RESULT 14

PT0706 T-cell receptor beta chain V-D-J region (135-1DU) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PR0706

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PR0706

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-4 <PPEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Qy	8	SG	9
I	1		
D	2	SG	3

RESULT 15

PT0675 T-cell receptor beta chain V-D-J region (140-1AC) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PR0675

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PR0675

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-4 <PPEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c

Qy	8	SG	9
I	1		
D	2	SG	3

Search completed: April 21, 2003, 12:12:21
 Job time : 11.6667 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:07:25 ; Search time 6.33333 Seconds
 (without alignments)
 65.489 Million cell updates/sec

Title: US-09-580-018-9
 Perfect score: 10
 Sequence: 1 DAEFRHDSGY 10

Scoring table: Oligo Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues
 Word size : 0

Total number of hits satisfying chosen parameters: 346

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2	RE21_LITRU	RE21_LITRU	5	1	P82071 litoria rub
2	2	RE31_LITRU	RE31_LITRU	5	1	P82072 litoria rub
3	2	UXA4_CHLTR	UXA4_CHLTR	5	1	P38005 chlamydia t
4	2	FARP_MONEX	FARP_MONEX	6	1	P41966 monilezia ex
5	2	TRPL_PSEPU	TRPL_PSEPU	6	1	P36414 pseudomonas
6	2	UN06_CLOPA	UN06_CLOPA	6	1	P81351 clostridium
7	2	FAR1_ASCSU	FAR1_ASCSU	7	1	P31889 ascaris suu
8	2	UFO3_MOUSE	UFO3_MOUSE	7	1	P36411 mus musculu
9	2	AL17_CARMA	AL17_CARMA	8	1	P81820 carcinus ma
10	2	ALL5_CYDPO	ALL5_CYDPO	8	1	P82156 cydida pomon
11	2	CPD1_ENTFA	CPD1_ENTFA	8	1	P13269 enteroocccu
12	2	GLUR_HUMAN	GLUR_HUMAN	8	1	P02729 homo sapien
13	2	LCK4_LEUMA	LCK4_LEUMA	8	1	P21143 leucophaea
14	2	LCK5_LEUMA	LCK5_LEUMA	8	1	P19987 leucophaea
15	2	ORMY_ORCLI	ORMY_ORCLI	8	1	P82455 orconectes
16	2	PPK3_PERRAM	PPK3_PERRAM	8	1	P82618 periplaneta
17	2	UC26_MAIZE	UC26_MAIZE	8	1	P80632 zea mays (m
18	2	VGLI_HSV2B	VGLI_HSV2B	8	1	P81790 herpes simp
19	2	COXE_THOUB	COXE_THOUB	9	1	P80975 thunnus obe
20	2	DSIP_RABTU	DSIP_RABTU	9	1	P01158 orcyctolatus
21	2	FAR5_ASCSU	FAR5_ASCSU	9	1	P43170 ascaris suu
22	2	FAR6_CALVO	FAR6_CALVO	9	1	P41861 calliphora
23	2	FARP_CALFU	FARP_CALFU	9	1	P38495 callinectes
24	2	FIBB_MACFU	FIBB_MACFU	9	1	P19345 macraca fusc
25	2	FIBB_PAPAN	FIBB_PAPAN	9	1	P19344 papio anubi
26	2	IPYR_RHOVI	IPYR_RHOVI	20	0	P28992 rhodopseudo
27	2	MOSF_CLYJA	MOSF_CLYJA	9	1	P19853 clypeaster
28	2	MOSH_CLYJA	MOSH_CLYJA	9	1	P19852 clypeaster
29	2	NEUU_CAVPO	NEUU_CAVPO	9	1	P34966 cavida porce
30	2	NEUX_CAVPO	NEUX_CAVPO	20	0	P04277 homo sapien
31	2	OXYT_OCTVU	OXYT_OCTVU	20	0	P80027 octopus vul
32	2	TKLL_LOCMI	TKLL_LOCMI	9	1	P16223 locusta mig
33	2	TRP4_LEUMA	TRP4_LEUMA	20	0	P81736 leucophaea

ALIGNMENTS

RESULT 1						
ID	RE21_LITRU	STANDARD;	PRT;	5 AA.		
AC	P82071;				CC	SEQUENCE=SKIN SECRETION;
DT	15-JUN-2002 (Rel. 41, Created)				RA	Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
DT	15-JUN-2002 (Rel. 41, Last sequence update)				RA	Tyler M.J., Wallace J.C.,
DE	Rubellidin 2.1.				RT	"The structure of new peptides from the Australian red tree frog
OS	Litoria rubella (Desert tree frog)				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;				OC	Pelodytidae; Litoria.
NCBI_TaxID	104895;				OX	NCBIL_TaxID=104895;
RN					RL	Aust. J. Chem. 49:955-963 (1996).
RP					CC	-!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
RC					CC	-!- ACTIVITY.
TISSUE					CC	-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
DB					CC	-!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW					KW	Amphibian skin
SEQUENCE					SQ	SEQUENCE 5 AA; 626 MW; 6DD9C9C9CB10300000 CRC64;
Query Match					Query	Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity					Query	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches					Query	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2					Db	2 EF 3
3					Db	2 EF 3
RESULT 2						
ID	RE31_LITRU	STANDARD;	PRT;	5 AA.		
AC	P82072;				CC	SEQUENCE=SKIN SECRETION;
DT	15-JUN-2002 (Rel. 41, Created)				RA	Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
DT	15-JUN-2002 (Rel. 41, Last sequence update)				RA	Tyler M.J., Wallace J.C.,
DE	Rubellidin 3.1.				RT	"Litoria rubella' - the skin peptide profile as a probe for the study
OS	Litoria rubella (Desert tree frog)				RT	of evolutionary trends of amphibians."
CC					RL	Aust. J. Chem. 49:955-963 (1996).
-!-					CC	-!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
-!-					CC	-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
-!-					CC	-!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
-!-					KW	Amphibian skin
-!-					SQ	SEQUENCE 5 AA; 626 MW; 6DD9C9C9CB10300000 CRC64;
Query Match					Query	Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity					Query	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches					Query	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2					Db	2 EF 3
3					Db	2 EF 3
RESULT 3						
ID	RE31_LITRU	STANDARD;	PRT;	5 AA.		
AC	P82073;				CC	SEQUENCE=SKIN SECRETION;
DT	15-JUN-2002 (Rel. 41, Created)				RA	Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
DT	15-JUN-2002 (Rel. 41, Last sequence update)				RA	Tyler M.J., Wallace J.C.,
DE	Rubellidin 3.1.				RT	"Litoria rubella (Desert tree frog)
OS	Litoria rubella (Desert tree frog)				RT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;				OC	Pelodytidae; Litoria.
NCBI_TaxID	104895;				OX	NCBL_TaxID=104895;
RN					RL	Aust. J. Chem. 49:955-963 (1996).
RP					CC	-!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
RC					CC	-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
DB					CC	-!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW					KW	Amphibian skin
SEQUENCE					SQ	SEQUENCE 5 AA; 626 MW; 6DD9C9C9CB10300000 CRC64;
Query Match					Query	Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity					Query	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches					Query	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2					Db	2 EF 3
3					Db	2 EF 3

"The structure of new peptides from the Australian red tree frog '*Litoria rubella*', the skin peptide profile as a probe for the study of evolutionary trends of amphibians.",
Aust. J. Chem. 49:955-963 (1966).

-1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.

-1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

-1- MASS SPECTROMETRY: MW=655; METHOD=FAB.

Amphibian skin: Amidation.
MOD-RES 5 5 AMIDATION
SEQUENCE 5 AA: 655 MW: 71A9C9CB10300000 CRC64;

Query Match	Similarity	Score 1	Score 2	DB 1	Length 5	
Best Local	Similarity	20.0%	Score 2;	DB 1;	Length 5;	
Best Local	100.0%	100.0%	No.	1.1e+05		
2. conservative			No.	Mismatches	Indels	Gaps
3. conservative			No.	0	0	0

3 EF 4	3 EF	1 1	2 EF 3	
				RESULT 3
				XA4_CHLTR
D	UXAA_CHLTR	STANDARD;	PRT;	5 AA.
C	P38005;			
T	01-OCT-1994	(Rel. 30, Created)		
T	01-OCT-1994	(Rel. 30, Last sequence update)		
T	30-MAY-2000	(Rel. 39, Last annotation update)		
E	Unknown protein from 2D-page	from elementary body (Fragment).		
S	Chlamydia trachomatis.			
B	Bacteria; Chlamydiales;			
C	Chlamydiaceae; Chlamydia.			

[1] IN
PC SEQUENCE.
PA STRAIN=L2/434/Bu;
PA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
PA Comanducci M., Christianen G., Birkelund S., Vtreteou E., Ratti G.,
PA Pallini V.;
PA Submitted (SEP-1994) to the SWISS-PROT data bank.
PA - I - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PA PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
CC Siena-2DPAGE: P38005; -.
OR

六
七
八
九

Ob 2 SG 3

RESULT 4

AND MONICA STANDARD; PRT; 6 AA:

01-NOV-1995 (Re) 32 Created)

01 - NOV - 1995 (Rel. 32, Last sequence update)
 01 - NOV - 1997 (Rel. 35, Last annotation update)
 FMRamide-like neuropeptide GNFFRP-amide.
 DE

Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;

CYCOLOPHIDAE; Anoplocephalidae; Monlezid.
NCB# may be 28841.

[1] RNRN
RP
SEQUENCE:
MEDLINE=933112289; PubMed=8323531;
Mauli A.G.; Shaw C.; Hallon D.W.; Thim L.;
GNNFRERRR: a novel FMRFamide-immunoreactive peptide isolated from
the sheep tapeworm, *Moniezia expansa*.
Biochem. Biophys. Res. Commun. 193:1097-1060(1993).

```

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation
FT MOD-RES 6 6 AMIDATION.
SQ SEQUENCE 6 AA: 787 MW: 69D40929C4481000 CRC64;
Query Match 20.0% Score 2; DB 1; Length 6;
Best Local Similarity 100.0% Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;
QY 4 FR 5

```

Db 5 ER 4

```

RESULTS
TRPL_PSEPU STANDARD; PRT; 6 AA.
ID TRPL_PSEPU
AC P3614;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TrpA operon transcriptional activator (Fragment).
GN TRP.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=PPG1 C1S;
MENDINE=902350506; PubMedID=2503057.

```

RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of *Pseudomonas*
 RT putida.";
 RL Biochimie 71: 521-531 (1989).
 CC - I - FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF
 CC TRPB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC - I - SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.

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KW Tryptophan biosynthesis; Transcription regulation; Activator;

FT NON-TER - 6 6 MN;
SQ SEQUENCE 6 AA; 683 6 MN;
77672AA1EDD6F000 CRC64;

```

Query Match          20.0%; Score 2;  Ub 1; Length 9;
Best Local Similarity 100.0%; Prod. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

```

QX 6 HD 7

Bb 3 3 4

RESULT 6
 UN06-CLOPA
 ID -UN06-CLOPA
 AC P81-35-;
 DT 15-JUL-1998 (Rel. 36, Created)
 STANDARD; PRT; 6 AA.

DT	15-JUL-1998 (Rel. 36, Last sequence update)	DT	01-OCT-1994 (Rel. 30, Last sequence update)
DT	15-JUL-1998 (Rel. 36, Last annotation update)	DT	01-FEB-1995 (Rel. 31, Last annotation update)
DE	Unknown protein CP 6 from 2D-page (Fragment).	DE	Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
OS	Clostridium pasteurianum.	OS	Mus musculus (Mouse).
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OX	NCBI_TaxID=1501;	OX	NCBI_TaxID=10090;
RN	[1]	RN	[1]
RP	SEQUENCE.	RP	SEQUENCE.
RC	STRAIN=W;	RC	TISSUE=Fibroblast;
RX	MEDLINE=98291870; PubMed=9629918;	RX	MEDLINE=95009907; PubMed=7523108;
RA	Fleissner R.; Skjeldal L.;	RA	Wichter L.L., He C., Selkirk J.K., Merrick B.A., Patterson R.M.
RT	*Two-dimensional gel electrophoresis separation and N-terminal sequencing analysis of proteins from Clostridium pasteurianum W5.;"	RT	"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
RL	Electrophoresis 19:802-806(1998)	RL	Electrophoresis 15:735-745(1994).
CC	-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.	CC	-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
FT	NON_TER 6 6	FT	NON_TER 7 7
SQ	SEQUENCE 6 AA; 657 MW; 605B1D1CA5A8000 CRC64;	SQ	SEQUENCE 7 AA; 842 MW; 6AA72B1DDB1B1180 CRC64;
Query Match	20.0%; Score 2; DB 1; Length 7;	Query Match	20.0%; Score 2; DB 1; Length 7;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;	Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Matches	2; Conservative 0; Mismatches 0; Indels 0;	Matches	2; Conservative 0; Mismatches 0; Indels 0;
Qy	2 AE 3	Qy	2 AE 3
Db	1 AE 5	Db	1 AE 5
Db	4 AE 5	Db	4 AE 5
RESULT 7		RESULT 9	
FAR1_ASCSU	STANDARD; PRT; 7 AA.	ALL17_CARMA	STANDARD; PRT; 8 AA.
ID	P31899;	ID	ALL17_CARMA
AC	DT 01-JUL-1993 (Rel. 26, Created)	AC	P81820;
DT	01-JUL-1993 (Rel. 26, Last sequence update)	DT	30-MAY-2000 (Rel. 39, Created)
DT	01-FEB-1996 (Rel. 33, Last annotation update)	DT	30-MAY-2000 (Rel. 39, Last sequence update)
DE	FMRamide like neuropeptide AF1.	DE	30-MAY-2000 (Rel. 39, Last annotation update)
AScaris suum (Pig roundworm) (Ascaris lumbricoides).	Ascaris suum (Pig roundworm) (Ascaris lumbricoides).	DE	Carcinus maenas (Common shore crab) (Green crab).
OC	Eukaryota; Metazoa; Nemata; Chromadorea; Ascaridoidea; Ascarididae; Ascaris.	OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Malacostraca; Eumalacostraca; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunidae; Carcinus.
NCBI_TaxID=6253;	NCBI_TaxID=6253;	NCBI_TaxID=6759;	NCBI_TaxID=6759;
RN	[1]	RN	[1]
RP	SEQUENCE.	RP	SEQUENCE.
RX	MEDLINE=90180465; PubMed=2627377;	RC	TISSUE=cerebral ganglion, and thoracic ganglion;
RA	Cowden C., Stretton A.O.W., Davis R.E.;	RX	MEDLINE=98121193; PubMed=9461295;
RT	"AF1, a sequenced bioactive neuropeptide isolated from the nematode Ascaris suum."	RA	Dave H., Johansen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
RT	Ascaris suum.;	RT	"Isolation and identification of multiple neuropeptides of the allatotropin superfamily in the shore crab <i>Carcinus maenas</i> .";
RL	Neuron 2:1465-1473 (1989).	RT	Eur. J. Biochem. 250:727-734 (1997).
CC	-!- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTORNEURONS REDUCES THE INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE CELLS.	CC	-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC	-!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.	CC	-!- SIMILARITY: BELONGS TO THE ALLATOOSTRIN FAMILY.
CC	-!- SIMILARITY: BELONGS TO THE FARP (FMRFamide RELATED PEPTIDE) FAMILY.	KW	Neuropeptide; Amidation; Multigene family.
CC	Neuropeptide; Amidation.	FT	MOD_RES 8 8 AMIDATION (POTENTIAL).
FT	MOD_RES 7 7 AMIDATION.	SQ	SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;
SQ	SEQUENCE 7 AA; 953 MW; 69D40059CB144350 CRC84;	Query Match	20.0%; Score 2; DB 1; Length 8;
Query Match	20.0%; Score 2; DB 1; Length 7;	Best Local Similarity	100.0%; Pred. No. 1.1e+05;
Best Local Similarity	100.0%; Pred. No. 1.1e+05;	Matches	2; Conservative 0; Mismatches 0; Indels 0;
Matches	2; Conservative 0; Mismatches 0; Indels 0;	Qy	8 SG 9
Qy	3 EF 4	Db	1 SG 2
Db	1 EF 4	Db	1 EF 2
RESULT 8		RESULT 10	
UF03_MOUSE	STANDARD; PRT; 7 AA.	ALL5_CYPO	STANDARD; PRT; 8 AA.
ID	UF03_MOUSE	ID	ALL5_CYDPO
AC	P38641;	AC	P82156;
DT	01-OCT-1994 (Rel. 30, Created)	DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)	DT	30-MAY-2000 (Rel. 39, Last annotation update)

DE Cydiastratin 5.	RP SEQUENCE.
OS Cydia pomonella (Codling moth).	RX MEDLINE=7/2062338; PubMed=5126885;
OC Eukaryota; Mettzoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;	RX Lotc C.J.; Weiss J.B.;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;	RT "Identification in urine of a low-molecular-weight highly polar
OC Glycopeptide containing cysteinyl-galactose.";	RT Glycopeptide 123:25P-25P(1971).
OX NCBI_TaxID=82600;	CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
RN [1]	IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
RP	ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A
RC TISSUE=Larva;	CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
RX MEDLINE=98054539; PubMed=9392829;	CC PIR; A03188; XGH0ED.
RA Duv B., Johnson A.H., Maestro J.L., Scott A.G., Winsstanley D.,	DW
RA Davey M., East P.D., Thorpe A.;	KW Glycoprotein.
RT "Lepidopteran peptides of the illatostatin superfamily.";	FT CARBOHYD
CC Peptides 18:1301-1309(1997).	SEQUENCE 8 AA: 855 MW; C2D8/AA1F5B1E CRC64;
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.	Query Match 20.0%; Score 2; DB 1; Length 8;
KW Neuropeptide; Amidation.	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
FT MOD_RES 8 AA: 898 MN; 922879CABB58640D CRC64;	Mismatches 0; Indels 0; Gaps 0;
SQ SEQUENCE 8 AA:	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 GY 10	Qy 6 HD 7
Db 1	Db 5 HD 6
Db 3 GY 4	Db 5 HD 6
RESULT 13	RESULT 13
LCK4_LEUMA	LCK4_LEUMA
ID LCK4_LEUMA	STANDARD
AC P21143;	PRT;
AC P21143; P13269	8 AA.
STANDARD; PRT; 8 AA.	8 AA.
DT 01-MAY-1991 (Rel. 18, Created)	DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)	DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin IV (L-IV).	DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).	OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;	OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;	OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.	OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988; RN [1]	OX NCBI_TaxID=6988; RN [1]
RP SEQUENCE, AND SYNTHESIS.	RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;	RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;	RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of cephalomyotropins.";	RT "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of cephalomyotropins.";
RT Comp. Biochem. Physiol. 84C:271-276(1986).	RT Comp. Biochem. Physiol. 84C:271-276(1986).
CC -!- FUNCTION: THIS CEPHALOMOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODERM (HINDGUT).	CC -!- FUNCTION: THIS CEPHALOMOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODERM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.	CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.	KW Neuropeptide; Amidation.
FT MOD_RES 8 AA: 906 MW; DC6365B1E9D5BDPA CRC64;	FT MOD_RES 8 AA: 906 MW; DC6365B1E9D5BDPA CRC64;
SQ SEQUENCE	SEQUENCE
Query Match 20.0%; Score 2; DB 1; Length 8;	Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 SG 9	Qy 1 DA 2
Db 1	Db 1 DA 2
Db 7 SG 8	Db 1 DA 2
RESULT 14	RESULT 14
LCK5_LEUMA	LCK5_LEUMA
ID LCK5_LEUMA	STANDARD
AC P19987;	PRT;
AC P19987; P02729	8 AA..
STANDARD; PRT; 8 AA..	8 AA..
DT 01-FEB-1991 (Rel. 17, Created)	DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)	DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin V (L-V).	DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).	OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;	OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;	OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.	OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=9606; RN [1]	OX NCBI_TaxID=9606; RN [1]

OX NCBI_TaxID=6988;
 RN [1]
 RP
 SEQUENCE.
 RC TISSUE=Head;
 RX MEDLINE=87052651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 "Isolation, primary structure, and synthesis of leucokinins V and VI:
 myoTropic peptides of Leucophæa maderae.";
 RT Comp. Biochem. Physiol. 88C:27-30(1987).
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 ACTIVITY OF COCKROACH PROTOPODUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 CC PIR: JS015; JS0315.
 DR Neuropeptide; Amidation.
 KW
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	8	SG	9
Db	2	SG	3

RESULT 15

ORMY_ORCLI STANDARD PRT: 8 AA.

ID ORMY_ORCLI
 AC P82455;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DR 16-Oct-2001 (Rel. 40, Last annotation update)
 DE Orcomyotropin (OMT).
 OS Orconectes limosus (Spinycheek crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Astacidea; Astacoidea; Cambaridae; Orconectes.
 QX NCBI_TaxID=28379;

OX [1]
 RP SPECTROMETRY, AND AMIDATION.
 RC TISSUE-Hindgut;
 RX MEDLINE=20411310; PubMed=10952880;
 RA Dirckxen H., Burdzik S., Sauter A., Keller R.;
 "Two orconectins and the novel octapeptide orconectyotropin in the hindgut
 of the crayfish Orconectes limosus: identified myostimulatory
 neuropeptides originating together in neurones of the terminal
 abdominal ganglion."
 RL J. Exp. Biol. 203:2807-2818 (2000).
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. ENHANCES BOTH THE FREQUENCY AND
 AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
 BY ABDOMINAL GANGLIONIC NEURONS.
 CC -!- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
 KW Amidation; Neuropeptide.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 905 MW; 87C861B19CDDAA9 CRC64;

Query Match Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DA	2
Db	2	DA	3



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GenCore version 5.1.4-p5-4578

protein - protein search, using sw model

run on: April 21, 2003, 12:07:50 ; Search time 22 Seconds
(without alignments)

scoring table: Oligo Gapop 60.0 , Gapext 60.0

title: US-09-580-018-9

perfect score: 10

sequence: 1 DAEFRHDSGY 10

searched: 671580 seqs, 200647115 residues

word size : 0

total number of hits satisfying chosen parameters: 1224

minimum DB seq length: 0

maximum DB seq length: 10

post-processing: Listing first 45 summaries

summary 21-45

Q9r5r2	shigella	dy
Q9r3x0	planktothri	
Q9r5l7	ciliostroidium	
Q8rsr3	lactobacil	
Q9urb9	saccharomy	c
Q9ur99	homo	sapien
Q15901	homo	sapien
Q9y4j4	homo	sapien
Q16428	homo	sapien
Q60773	homo	sapien
Q9ub13	albinaria	h
Q94623	manduca	sex
P82686	periplaneta	
Q9my15	pongo	pygma
Q9gmh3	ligenorhinc	
Q28866	megaptera	n
Q8wns1	bos	taurus
Q9bfc3	didelphis	m
Q9bic2	macropus	eu
Q9bfc1	choleopus	h
Q9bfc0	choleopus	d
Q9fb99	euphractus	
Q9fb8	chaetophrac	
Q9fb7	tamandua	te
Q9bbf6	myrmecophag	
Q9bbf5	erinaceus	c
Q9bb4	talpa	alta
Q9bb3	condylura	c
Q9bb2	storer	arane
Q9bb1	echinops	te

DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)	DE glycosidase) (N-glycanase) (Fragment).
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	OS <i>Prunus dulcis</i> (Almond) (<i>Prunus amygdalus</i>).
DE	Putative glucokinase (fragment).	OC Fukarava; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta;
GLK		OC Spermatophita; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
GN		OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OS		OX NCBI_TAXID=3755;
OC		RN [1]
OC	Pseudomonas aeruginosa.	RP SEQUENCE, AND CHARACTERIZATION.
OC	Bacteriorhizobacteria; gamma subdivision; Pseudomonadaceae;	RX PubMed=9523720;
OC	Pseudomonas	RX Altmann F., Paschinger K., Dalik T., Vorauer K.;
OX		RA "Characterization of Peptide-N-(N-acetyl-beta-D-glucosaminyl)asparagine amidase A and its N-glycans.";
RN		RT Eur. J. Biochem. 252:118-123 (1998).
RC	SEQUENCE FROM N.A.	RL -1- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE CONTAINING AN ASPARTIC RESIDUE.
RX	CHARACTERIZATION	CC -1- SUBUNITS: HETERODIMER OF A LARGE AND A SMALL CHAIN.
RX	"Characterization"	CC -1- PRM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-DEGLYCOSYLATION.
RX	"Characterization"	CC -1- MASS SPECTROMETRY: MW=54182; METHOD=MALDI-MS.
RX	"Characterization"	KW Hydrolase; Glycoprotein.
RX	"Characterization"	FT NON_TER 10 10
RX	"Characterization"	SQ SEQUENCE 10 AA; 1106 MW; 95F6BF65B1FB5865 CRC64;
RESULT 3		Query Match 30.0%; Score 3; DB 2; Length 9;
Q9TU33	Q9TU33	Best Local Similarity 100.0%; Pred. No. 6.7e+05; Mismatches 0; Indels 0; Gaps 0;
AC	Q9TU33;	PRT; 10 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)	RESULT 5
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	Q9J1G8
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	PRELIMINARY; PRT; 10 AA.
DE	BRCA1 (Fragment).	ID Q9J1G8
GN	BRCA1.	AC Q9J1G8;
OS	Canis familiaris (Dog).	DT 01-OCT-2000 (TREMBLrel. 15, Created)
OC	Chordata; Craniata; Vertebrata; Euteleostomi;	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
QC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
OX		DE ORF2.
RN	[1]	OS TTV virus.
RP	SEQUENCE FROM N.A.	OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
RX	MEDLINE=2015495; PubMed=10650375;	OX NCBI_TAXID=88887;
RA	Gray T.S., Yuzbasyan-Gurkan V.	RN [1]
RT	"A single nucleotide (T-->G) polymorphism within intron 23 of the canine BRCA1 gene."	RP SEQUENCE FROM N.A.
RT	Anim. Genet. 31:76-77 (2000).	RC STRAIN=T7V-SC232;
RL	DR EMBL_AF159258; AAD56289; 1. -	RX MEDLINE=20251008; PubMed=10790123;
FT	NON_TER 1 1	RA Niel C., Saback F.L., Lampe E.;
FT	NON_TER 10 10	RT Coinfection with Multiple TTV Strains Belonging to Different Genotypes Is a Common Event in Brazilian Healthy Adults.";
SQ	SEQUENCE 10 AA; 1164 MW; 2AB89C65BAAB01B3 CRC64;	RL J. Clin. Microbiol. 38:1926-1930 (2000).
Query Match 30.0%; Score 3; DB 6; Length 10;	DR AF216453; AAF66489; 1. -	
Best Local Similarity 100.0%; Pred. No. 4.3e+03; Mismatches 0; Indels 0; Gaps 0;	SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD71B5B9CB CRC64;	
Q9TU33	Q9TU33	Query Match 30.0%; Score 3; DB 12; Length 10;
AC	Q9TU33;	Best Local Similarity 100.0%; Pred. No. 4.3e+03; Mismatches 0; Indels 0; Gaps 0;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	RESULT 4
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	P81899
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	PRELIMINARY; PRT; 7 AA.
DE	Peptide-N4-(N-acetyl-beta-D-glucosaminyl)asparagine amidase A, large chain (Subunit A) (EC 3.5.1.52) (PGNase A) (Glycopeptide N-	ID Q47477
DE	(Subunit A) (EC 3.5.1.52) (PGNase A) (Glycopeptide N-	AC Q47477;
DE	(Subunit A) (EC 3.5.1.52) (PGNase A) (Glycopeptide N-	DT 01-NOV-1996 (TREMBLrel. 01, Created)
DE	(Subunit A) (EC 3.5.1.52) (PGNase A) (Glycopeptide N-	DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE	(Subunit A) (EC 3.5.1.52) (PGNase A) (Glycopeptide N-	DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)

DE Tpi protein (Fragment).
 GN Escherichia coli.
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC
 OX NCBI_TAXID=522;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85203917; PubMed=3158524;
 RA Hellenga H.W., Evans P.R.;
 "Nucleotide sequence and high-level expression of the major
 Escherichia coli phosphofructokinase.";
 RT Eur. J. Biochem. 149:363-373(1985).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA Evans P.;
 RL Submitted (Oct-1986) to the EMBL/GenBank/DBJ databases.
 DR X02519; CAA26359.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;
 Query Match 20.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 2 AE 3
 Db 1 AE 2
 RESULT 7
 ID Q15897 PRELIMINARY; PRT; 7 AA.
 AC Q15897;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE (clone XP611A) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 Caskey C.T.H.;
 "Isolation of chromosome-specific genes by reciprocal probing of
 arrayed cDNAs and cosmid libraries.";
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL; L32077; AAA73887.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;
 Query Match 20.0%; Score 2; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 2 AE 3
 Db 5 AE 6
 RESULT 8
 ID Q28742 PRELIMINARY; PRT; 7 AA.
 AC Q28742;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Alpha-myosin heavy chain (Fragment).

OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TAXID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84221901; PubMed=6328491;
 RA Friedman D.J., Umehara P.K., Sinha A.M., Hsu H.-J., Jokovicic S.,
 Rabinowitz M.;
 "Characterization of genomic clones specifying rabbit alpha- and beta-
 ventricular myosin heavy chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
 DR EMBL; K01698; AAA31415.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;
 Query Match 20.0%; Score 2; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 6 HD 7
 Db 4 HD 5
 RESULT 9
 ID Q98866 PRELIMINARY; PRT; 7 AA.
 AC Q98866;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE Cytochrome b/f subunit IV (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Chloroplast;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 NCBI_TAXID=3562;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=3003688;
 RX MEDLINE=86120353;
 RA Sijben-Muellem G., Hallik R.B., Alt J., Westhoff P., Herrmann R.G.;
 "Spinach plastid genes coding for initiation factor IF-1, ribosomal RNA,
 protein S11 and RNA polymerase alpha-subunit.";
 RT Nucleic Acids Res. 14:1029-1044(1986).
 RL EMBL; X03196; CAA27215.1; -.
 KW Chloroplast;
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 901 MW; 644729D774090420 CRC64;
 Query Match 20.0%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 4 FR 5
 Db 2 FR 3
 RESULT 10
 ID Q55184 PRELIMINARY; PRT; 7 AA.
 AC Q55184;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Orphan receptor TR4 NS (Fragment).
 GN TR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.
 NCBI_TAXID=10116;

[1]	SEQUENCE FROM N.A. STRAIN=SPAGUE-DAWLEY; MEDLINE=9619847; PubMed=8612486; RA Yoshioka T., Makino S., Gao X.M., Xing G.Q., Chuang D.M., RA Detera-Wadleigh S.D.; RT "splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal domain."; RT Endocrinology 137:1562-1571(1996). RL RN	DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update) DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update) DE Cytochrome b (Fragment) GN PETB.
[2]	SEQUENCE FROM N.A. STRAIN=SPAGUE-DAWLEY; MEDLINE=96299786; PubMed=8661150; RA Yoshioka T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.; RT "New variants of the human and rat nuclear hormone receptor, TR4: expression and chromosomal localization of the human gene."; RT Genomics 35:361-366(1996). EMBL; U59454; AAB91433.1; -. Kw Receptor. FT NON_TER 1 1 SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64; Query Match 20.0%; Score 2; DB 11; Length 7; Best Local Similarity 100.0%; Pred. No. 6.7e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 DA 2 Db 6 DA 7 RESULT 11 ID 068415 PRELIMINARY; PRT; 8 AA. AC 068485; PRELIMINARY; PRT; 8 AA. AC 068485; PRELIMINARY; PRT; 8 AA. DT 01-AUG-1998 (TREMBLrel. 07, Created) DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update) DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update) DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment). GN AADAI... Klebsiella pneumoniae. Plasmid pLQ1000. OG Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; OC Klebsiella. NCBI_TaxID=573; RN [1] SEQUENCE FROM N.A. STRAIN=KL1; MEDLINE=98287600; PubMed=9624504; RA Centro D., Roy P.H.; RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene aac(6')-Iq from the integron of a natural multiresistance plasmid."; RT aac(6')-Iq from the integron of a natural multiresistance plasmid."; EMBL; AF07556; AAC25501.1; -. KW Plasmid; Transferase. FT NON_TER 8 8 SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64; Query Match 20.0%; Score 2; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 6.7e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 2 AE 3 Db 3 AE 4 RESULT 12 ID Q9X3K1 PRELIMINARY; PRT; 8 AA. AC 09X3K1; PRELIMINARY; PRT; 8 AA. DT 01-FEB-1997 (TREMBLrel. 02, Created) DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DE Alignate lyase (Fragment). GN ALY. OS Pseudomonas sp. (strain OS-ALG-9). OC Bacteria; Proteobacteria. NCBI_TaxID=86338; OX OS	DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update) DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update) DE Cytochrome b (Fragment) GN PETB.
[3]	SEQUENCE FROM N.A. STRAIN=SPAGUE-DAWLEY; MEDLINE=9619847; PubMed=8612486; RA Yoshioka T., Makino S., Gao X.M., Xing G.Q., Chuang D.M., RA Detera-Wadleigh S.D.; RT "splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal domain."; RT Endocrinology 137:1562-1571(1996). RL RN	DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update) DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update) DE Cytochrome b (Fragment) GN PETB.
[4]	SEQUENCE FROM N.A. STRAIN=SPAGUE-DAWLEY; MEDLINE=96299786; PubMed=8661150; RA Yoshioka T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.; RT "New variants of the human and rat nuclear hormone receptor, TR4: expression and chromosomal localization of the human gene."; RT Genomics 35:361-366(1996). EMBL; U59454; AAB91433.1; -. Kw Receptor. FT NON_TER 1 1 SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64; Query Match 20.0%; Score 2; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 6.7e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 8 SG 9 Db 5 SG 6 RESULT 13 ID Q9S6D5 PRELIMINARY; PRT; 8 AA. AC 09S6D5; PRELIMINARY; PRT; 8 AA. DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DE Putative IS30 transposase (Fragment). OS Escherichia coli. OC Escherichia. NCBI_TaxID=562; RN [1] SEQUENCE FROM N.A. RC STRAIN=A295B; RX MEDLINE=90194747; PubMed=10094716; RA Rahm A., Drummondsmith J., Whitfield C.; RT "Conserved organization in the cps gene clusters for expression of Escherichia coli group I K antigens: relationship to the colanic acid biosynthesis locus and the cps genes from Klebsiella pneumoniae."; RT Escherichia coli. RL EMBL; AF118251; AAD300083.1; -. DR EMBL; AF118251; AAD300083.1; -. FT NON_TER 8 8 SQ SEQUENCE 8 AA; 1011 MW; F21DC1A9D1B41406 CRC64; Query Match 20.0%; Score 2; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 6.7e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 2 AE 3 Db 7 AE 8 RESULT 14 ID P72221 PRELIMINARY; PRT; 8 AA. AC P72221; PRELIMINARY; PRT; 8 AA. DT 01-FEB-1997 (TREMBLrel. 02, Created) DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DE Alignate lyase (Fragment). GN ALY. OS Pseudomonas sp. (strain OS-ALG-9). OC Bacteria; Proteobacteria. NCBI_TaxID=86338; OX OS	DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update) DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update) DE Cytochrome b (Fragment) GN PETB.

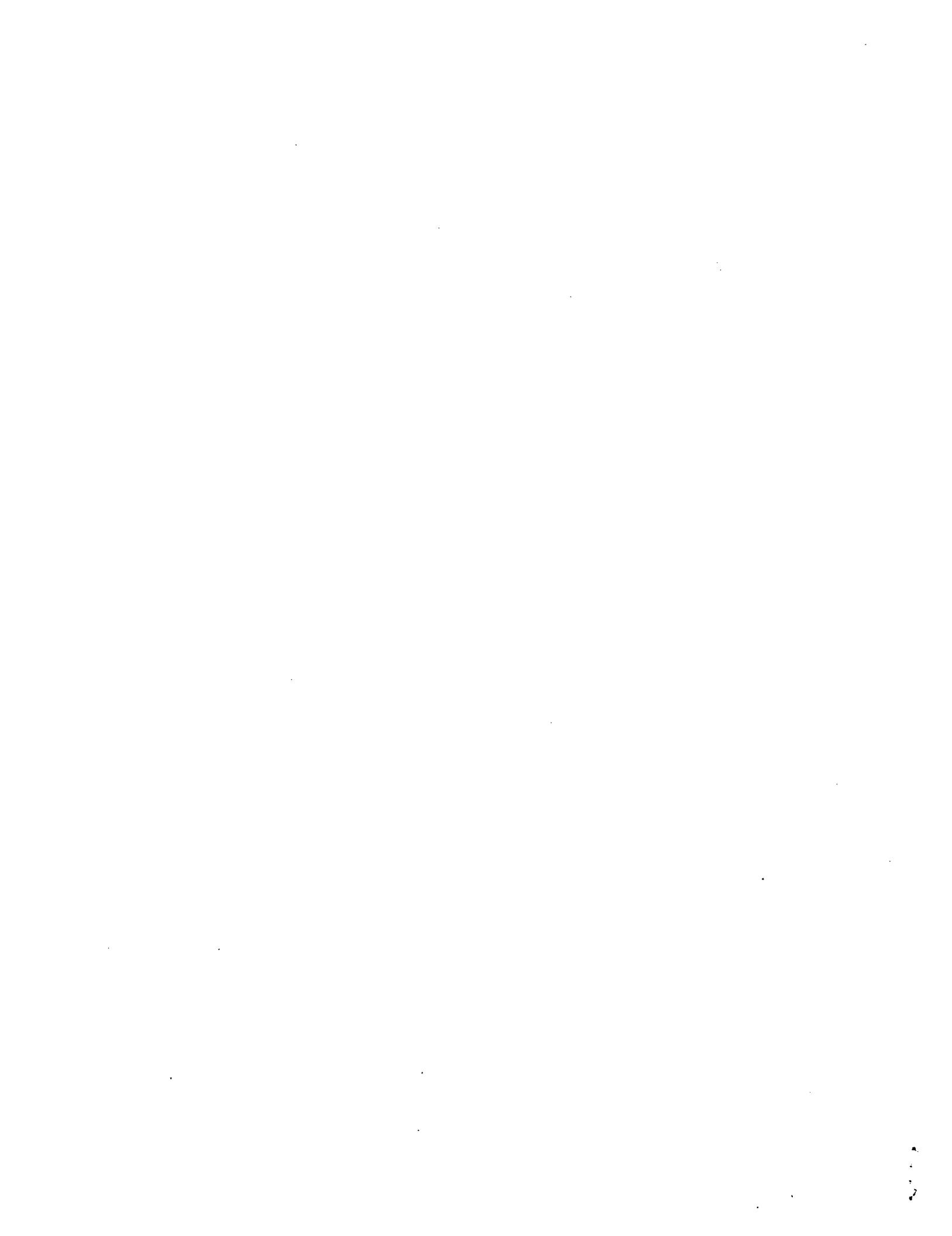
[1] RN
SEQUENCE FROM N.A.
STRAIN=OS-ALG-9;
RC Fujiyama K.;
RA Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
[2] RN
SEQUENCE FROM N.A.
STRAIN=OS-ALG-9;
RC PMID=93329366; PubMed=33613;
RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
RT "Cloning, sequence analysis and expression in Escherichia coli of a
gene encoding an alginate lyase from Pseudomonas sp. OS-ALG-9.";
RL J. Gen. Microbiol. 139:987-993(1993).
DR EMBL; D38469; BAA21704.1; -
KW Lyase.
FT NON_TER
FT NON_TER 1 1
FT 8 AA; 841 MW; 461DDDC5A5B041BB CRC64;
SQ SEQUENCE 8 AA; 8 8

Query Match Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2 AE 3
Db	7 AE 8

RESULT 15
Q9RT2 PRELIMINARY; PRT; 8 AA.
ID Q9RT2
AC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 1.0 kDa protein (Fragment).
GN YQFG.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBL-TaxID=552;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Rajai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishi Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiechi T.;
RT "A 718-kb DNA sequence of Escherichia coli K-12 Genome Corresponding
to the 12.7-28.0 min Region on the Linkage Map.";
RL DNA Res. 3:137-155(1996);
DR EMBL; D90705; BAA35310.1; -
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;
Query Match Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2 AE 3
Db	5 AE 6



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 11:57:04 ; Search time: 36 Seconds

(without alignments)
155.459 Million cell updates/sec

Perfect score: US-09-580-018-42

Sequence: 1 DAEFRHDSGYEVHKLVFF.....DVGSNKGAIIGLMYGGVYIA 42

Scoring table: BLOSUM62

gapop 10.0 , Gapext 0.5

Searched: 908470 seqs., 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002:*

1: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1980.DAT;*: 2: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1981.DAT;*: 3: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1982.DAT;*: 4: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1983.DAT;*: 5: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1984.DAT;*: 6: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1985.DAT;*: 7: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1986.DAT;*: 8: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1987.DAT;*: 9: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1988.DAT;*: 10: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1989.DAT;*: 11: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1990.DAT;*: 12: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1991.DAT;*: 13: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1992.DAT;*: 14: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1993.DAT;*: 15: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1994.DAT;*: 16: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1995.DAT;*: 17: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1996.DAT;*: 18: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1997.DAT;*: 19: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1998.DAT;*: 20: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA1999.DAT;*: 21: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA2000.DAT;*: 22: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA2001.DAT;*: 23: /SIDS2/gcdata/geneseq/geneseqp-emb1/AA2002.DAT;*: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	217	100.0	42	13	AFB20330	Sequence of A99 (b
2	217	100.0	42	15	AFB0366	Beta-amyloid (1-42
3	217	100.0	42	17	AAR95248	Beta/A4 amyloid pe
4	217	100.0	42	17	AAR94591	Alzheimer amyloid
5	217	100.0	42	18	RAW12828	Beta A4 Peptide.
6	217	100.0	42	19	AAR64507	Neurotoxic beta am
7	217	100.0	42	19	AAR47230	Beta-amyloid peptide
8	217	100.0	42	19	AAR42989	Full length beta-a
9	217	100.0	42	20	AAY49691	Human beta amyloid
10	217	100.0	42	20	AAY33407	Human amyloidogeni

RESULT 1	XX	XX	XX	XX	XX	XX
AAR20330	ID	AAR20330	standard; peptide;	42 AA.		
	XX	XX				
	AC	AAR20330;				
	DT	14-APR-1992	(first entry)			
	XX	XX				
	DE	Sequence of A99 (beta-amyloid core domain).				
	XX	XX				
	KW	transgenic mice; Alzheimer's disease; diagnosis;				
	XX	XX				
	OS	Homo sapiens.				
	XX	XX				
	PN	W09119810-A.				
	PD	26-DEC-1991.				
	PP	17-JUN-1991;	91WO-US04447.			
	PR	15-JUN-1990;	9005-0538857.			
	XX	XX				
	(CALB)	CALIF BIOTECHN INC.				
	XX	XX				
	PI	CordeLL B;				
	XX	XX				
	DR	WPI; 1992-024426/03.				
	PT	Transgenic mice as models for studying Alzheimer's disease				
	PT	proteins - contg. cells with promoter and beta-amyloid precursor				
	PT	protein deoxyribonucleic acid, useful for testing				
	PT	anti-alzheimer's drugs				

XX	PS Disclosure; Fig 3; 98pp; English.	Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42	Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
CC	The inventors specifically claim transgenic mice contg. DNA encoding A42 (beta-amyloid precursor protein) (AAR20330), A99 (beta-amyloid carboxy tail) (AAR20329), A695 (beta-amyloid precursor protein), A751 (precursor plus inhibitor) or A41 (protease inhibitor) (AAR20328).	RESULT 3 ID AAR95248 ID AAR95248 standard; peptide; 42 AA.	
CC	Human fibroblast cDNA clone lambdaAPC168i4 was deposited at ATCC on July 1, 1987 and has accession No. 40347. The promoter is pref. the NSE promoter with the A751 or the A695 sequence.	XX	
XX	Sequence 42 AA;	AC AAR95248; XX 20-JAN-1997 (first entry)	AC AAR95248; XX 20-JAN-1997 (first entry)
Query Match 100.0%; Score 217; DB 13; Length 42;	Best Local Similarity 100.0%; Pred. No. 8.2e-25; Indels 0; Gaps 0;	DE Beta/A4 -amyloid peptide.	DE Beta/A4 -amyloid peptide.
Best Local Similarity 100.0%; Pred. No. 8.2e-25;	Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX Beta/A4 -amyloid peptide; tissue plasminogen activator; Alzheimer's disease; stimulation; investigation; pathogenesis; hereditary cerebral hemorrhage with amyloidosis-Dutch type; control; cerebral amyloid angiopathy; cerebral haemorrhage; hemorrhage.	XX Beta/A4 -amyloid peptide; tissue plasminogen activator; Alzheimer's disease; stimulation; investigation; pathogenesis; hereditary cerebral hemorrhage with amyloidosis-Dutch type; control; cerebral amyloid angiopathy; cerebral haemorrhage.
XX	AC AAR60366;	XX Homo sapiens.	XX Homo sapiens.
XX	AC AAR60366;	XX WO9615799-A1.	OS
XX	DT 15-MAR-1995 (first entry)	XX WO9615799-A1.	XX
XX	DE Beta-amyloid (1-42).	XX PD 30-MAY-1996.	PN 30-MAY-1996.
XX	XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid; anil-beta-amyloid antibody; diagnosis.	XX PF 22-NOV-1995;	PF 22-NOV-1995;
XX	XX KW	XX PR 22-NOV-1994;	PR 22-NOV-1994;
XX	XX KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid; anil-beta-amyloid antibody; diagnosis.	XX PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.	PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX	XX OS Homo sapiens.	XX PI Anderson S;	PI Anderson S;
XX	XX PN WO9417197-A.	XX DR 1996-268332/27.	XX DR 1996-268332/27.
XX	XX PD 04-AUG-1994.	XX XX use of agents which bind beta-amyloid peptide - for diagnosis, prevention and treatment of vascular damage caused by amyloid deposits, partic. in haemorrhaging and Alzheimer's disease	XX XX use of agents which bind beta-amyloid peptide - for diagnosis, prevention and treatment of vascular damage caused by amyloid deposits, partic. in haemorrhaging and Alzheimer's disease
XX	XX PF 24-JAN-1994;	XX PS Example 1; Fig 1; 52pp; English.	XX PS Example 1; Fig 1; 52pp; English.
XX	XX PN 94WO-JP00089;	XX CC To investigate the effects of beta-amyloid peptide (BAP) on tissue plasminogen activator (t-PA) 3 synthetic peptides were used.	XX CC To investigate the effects of beta-amyloid peptide (BAP) on tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
XX	XX PR 25-JAN-1993;	CC One peptide contained 42 amino acids and corresp. to the full length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained the 38 N-terminal residues of the BAP found in Alzheimer's disease and hereditary cerebral haemorrhage with amyloidosis-Dutch type (HCHWA-D), respectively. In an assay to determine the effect of the peptides on t-PA activation, each peptide (AAR95248, 49 and 50) gave 1st order rate constant of activation (k_{app}) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for nil DR and fibrinogen controls. The results demonstrate that the BAP are able to stimulate t-PA activity in vitro, which is significant in that it provides a means for investigating and controlling the pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid angiopathy related cerebral haemorrhage.	CC One peptide contained 42 amino acids and corresp. to the full length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained the 38 N-terminal residues of the BAP found in Alzheimer's disease and hereditary cerebral haemorrhage with amyloidosis-Dutch type (HCHWA-D), respectively. In an assay to determine the effect of the peptides on t-PA activation, each peptide (AAR95248, 49 and 50) gave 1st order rate constant of activation (k_{app}) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for nil DR and fibrinogen controls. The results demonstrate that the BAP are able to stimulate t-PA activity in vitro, which is significant in that it provides a means for investigating and controlling the pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid angiopathy related cerebral haemorrhage.
XX	XX PR 05-FEB-1993;	CC Sequence; Page 83; 116pp; Japanese.	CC Sequence; Page 83; 116pp; Japanese.
XX	XX PR 16-NOV-1993;	XX DR WPI, 1994-264110/32.	XX DR WPI, 1994-264110/32.
XX	XX PR 28-DEC-1993;	XX Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as Alzheimer's disease	XX Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as Alzheimer's disease
XX	XX PA (TAKEDA CHEM IND LTD.	XX PS	XX PS
XX	XX PI Kitada C, Odaka A, Suzuki N;	XX DR	XX DR
XX	XX XX Disclosure; Page 83; 116pp; Japanese.	XX DR	XX DR
XX	CC Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's disease.	CC Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's disease.	CC Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's disease.
XX	CC Sequence 42 AA;	CC SQ sequence 42 AA;	CC SQ sequence 42 AA;
XX	CC Query Match 100.0%; Score 217; DB 17; Length 42;	CC SQ Query Match 100.0%; Score 217; DB 17; Length 42;	CC SQ Query Match 100.0%; Score 217; DB 17; Length 42;
CC	CC Best Local Similarity 100.0%; Pred. No. 8.2e-25; Indels 0; Gaps 0;	CC Best Local Similarity 100.0%; Pred. No. 8.2e-25; Indels 0; Gaps 0;	CC Best Local Similarity 100.0%; Pred. No. 8.2e-25; Indels 0; Gaps 0;
CC	CC Matches 42; Conservative 0; Mismatches 0;	CC Matches 42; Conservative 0; Mismatches 0;	CC Matches 42; Conservative 0; Mismatches 0;
CC	CC Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42	CC Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42	CC Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
CC	CC RESULT 4 ID AAR94591	CC	CC RESULT 4 ID AAR94591

ID	AAR94591	standard; peptide; 42 AA.	PN	WO9707403-A1.
XX	AC		XX	
XX	XX		PD	27-FEB-1997.
DT	21-AUG-1996	(first entry)	XX	
XX	XX		PF	23-JUL-1996;
DE	Alzheimer amyloid beta-protein active site sequence.		XX	96WO-US12034.
XX			PR	16-AUG-1995;
XX			XX	95US-0515606.
KW	Beta amyloid; Alzheimer's disease; cholinesterase; lipase; ebelactone-A;		XX	(HMRI) HOECHST MARION ROUSSEL INC.
KW	Serine protease; para-amidinophenylmethanesulphonyl fluoride; inhibition;		PA	
KW	Complex formation; alpha(1)-antichymotrypsin; Down's diseases; ageing.		XX	
XX			PI	Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;
OS	Synthetic.		XX	
XX			DR	WPI: 1997-165447/15.
PN	US5506097-A.		XX	
XX	XX	Determn. of the degree of betaA4 peptide aggregation using binding	PT	
PD	09-APR-1996.	agent - used to screen cpds. for possible use in Alzheimer's disease	PT	
XX			PT	treatment
PF	24-AUG-1990;	90US-0572671.	XX	
XX			PS	
PR	10-JAN-1994;	94US-0179574.	XX	
PR	24-AUG-1990;	90US-0572671.	XX	This sequence represents the beta A4 peptide. The degree of aggregation
PR	13-JAN-1992;	92US-0819361.	CC	of this peptide is determined using the method of the invention. The beta
PR	13-JAN-1993;	93WO-US00325.	CC	A4 peptide is present in the brain of Alzheimer's disease patients, but
XX			CC	not in the brain of non-Alzheimer's disease individuals. The peptide
PA	(HARD) HARVARD COLLEGE.		CC	clumps or aggregates in the brain of Alzheimer's disease patients, where
XX			CC	it may be responsible for the destruction of normal brain cells. Once the
PI	Kayali U, Potter H;		CC	clumps or aggregates form, the formulation is almost irreversible. The
XX			CC	method of the invention comprises reacting this sequence with a binding
DR	WPI: 1996-200270/20.		CC	agent capable of binding to it only in its non-aggregated state, to
XX			CC	form an amount of a beta A4 peptide-bound reagent and an amount of
PT	Inhibiting enzymatic activity of Alzheimer amyloid beta-protein -		CC	protein free reagent. The amount of the beta A4 peptide, binding reagent
PT	Using p-amidino:phenylmethanesulphonyl fluoride or ebelactone A,		CC	complex is then measured. Compounds which inhibit aggregation of beta A4
PT	for treatment, study and diagnosis of Alzheimer's disease, etc.		CC	peptide are potentially useful for treatment of Alzheimer's disease.
PS	Disclosure; Fig 1; 17pp; English.		XX	
XX			SQ	Sequence 42 AA;
CC	This is the sequence of a fragment of the beta-amyloid protein		Query Match	Score 217; DB 18; Length 42;
CC	associated with Alzheimer's disease. The protein contains esterase		Best Local Similarity	100.0%; Pred. No. 8.2e-25;
CC	(cholinesterase and lipase) activities based on active site similarities		Matches 4;	Mismatches 0; Indels 0; Gaps 0;
CC	with serine proteases (see AAR9592-96). The esterase activity of the		AC	
CC	beta-amyloid protein is inhibited by the cpds. of the invention i.e.		XX	
CC	ebelactone A or para-amidinophenylmethanesulphonyl fluoride.		AC	
CC	Inhibition of these activities prevent complex formation between the beta-amyloid		XX	
CC	protein and alpha(1)-antichymotrypsin, thus can be used to treat, study		DE	
CC	or diagnose Alzheimer's or Down's diseases or normal ageing.		XX	
XX			KW	Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;
XX			XX	aggregate; Alzheimer's disease; decoy; treatment.
SQ	Sequence 42 AA;		XX	
Query Match	100.0%; Score 217; DB 17; Length 42;		OS	Synthetic.
Best Local Similarity	100.0%; Pred. No. 8.2e-25;		XX	
Matches 4;	0; Mismatches 0; Indels 0; Gaps 0;		AC	
XX			XX	
AC			DT	20-OCT-1998 (first entry)
AC			XX	
AC	AAW12828;		XX	
XX	XX		XX	
XX	XX		XX	
DT	08-DEC-1997 (first entry)		XX	
XX	Beta A4 peptide.		XX	
DE			PR	29-OCT-1997; 97US-0960188.
XX			PR	10-JAN-1997; 97US-0035847.
XX			PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.
XX			XX	
OS	Homo sapiens.		PI	Blanchard BJ, Ingram VM;
XX			XX	

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
RESULT 9
AAY49691 standard; peptide; 42 AA.
ID AAY49691
XX
AC AAY49691;
XX DT 13-JAN-2000 (first entry)
XX Human beta amyloid precursor protein peptide.
DE
XX Human; beta amyloid precursor protein; APP; beta secretase inhibition;
KW alpha secretase; neurological disorder; Alzheimer's disease;
KW Down syndrome; mutation.
XX
OS Homo sapiens.
XX PN WO9951752-A1.
XX PD 14-OCT-1999.
XX PF 31-MAR-1999; 99WO-JP01701.
XX PR 31-MAR-1998; 98JP-0101821.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Ozawa K, Ikeda S, Tabira T;
XX DR WPI; 1999-620208/53.
PT A cell line which produces beta amyloid precursor protein, used in the investigation of neurological disorders such as Alzheimer's disease .
XX
PS Disclosure; Page 41; 70pp; Japanese.
XX
CC The present invention describes a cell line which produces beta amyloid precursor protein (APP) and expresses alpha secretase activity but expresses beta secretase activity only under an external stimulus.
CC Also described is a cloning method for DNA encoding beta secretase, comprising: (1) inserting a DNA library into the cell line, expressing the inserted DNA, and selecting cells expressing beta secretase then isolating the beta secretase DNA from them; or (2) isolating nucleic acid from the cell line with or without external stimulation and performing subtractive cloning to identify DNA expressed only under stimulation. Products from the present invention may be used in the investigation of neurological disorders such as Alzheimer's disease and Down's syndrome and in particular the association of mutations of the beta APP with them. The present sequence represents a human beta APP peptide.
XX Sequence 42 AA;
SQ Query Match 100.0%; Score 217; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 8 2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DE
XX
AC AAY25137;
XX DT 26-AUG-1999 (first entry)
XX Human amyloid beta-A4 peptide 5.
DE
XX
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIA 42
XX Sequence 42 AA;
SQ Query Match 100.0%; Score 217; DB 20; Length 42;
Best Local Similarity 100.0%; Pred. No. 8 2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DE
XX
AC AAY33407;
XX DT 03-DEC-1999 (first entry)
XX DE Human amyloidogenic A-beta peptide 1.
XX

RESULT 10
AAY33407
ID AAY33407 standard; peptide; 42 AA.
XX
AC AAY33407;
XX DT 17-JUL-1996; 96US-0682245.
XX PA (HMRI) HOECHST MARION ROUSSEL INC.
XX

PI Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;
 XX DR WPI: 1999-403957/34.

XX PT Determination of degree of aggregation of a peptide, useful for identifying therapeutic drugs for treating Alzheimer's disease

PT XX PS Claim 1; Column 7-8; 8pp; English.

XX This invention describes a novel method for the determination of the degree of aggregation of an amyloid beta A4 peptide (I) in solution. The determination comprises: (a) incubating a sample of unaggregated (I) with Coomassie Brilliant Blue G 250 dye (II) which only binds to unaggregated (I); (b) measuring the amount of (II) bound to (I) to obtain a value (I_b); (C) repeating steps (a) and (b) with a second sample at a different time to obtain a second value (II_b); and (d) determining the difference between (I_b) and (II_b) which is inversely related to the degree of aggregation of (I). This method may be applied to a screen for compounds that inhibit aggregation of (I). These inhibitors may be used as therapeutic drugs to inhibit the formation of these aggregates in the brains of patients suffering from Alzheimer's disease.

XX SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25; Indels 0; Gaps 0;

Matches 42; Conservative 0; Mismatches 0; Sequence 42 AA;

RESULT 13
 AAW29093 ID AAW29093 standard; peptide; 42 AA.
 AC AAW29093;
 XX DT 20-JUL-1999 (first entry)
 DE A-beta-binding peptide 1-42.
 XX KW Cyclosporin; A-beta peptide; conjugate; neurological disease; Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis; ALS; non-immunosuppressive; amyloid plaque formation.

XX OS Homo sapiens.
 PN WO9910374-A1.
 XX PR 04-MAR-1999.
 XX PF 25-AUG-1998; 98WO-US17544.
 XX DR 26-AUG-1997; 97US-0057751.
 XX PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX PI Rich DH, Solomon ME;
 XX DR WPI: 1999-276928/23.
 XX PS Claim 5; Page 98; 129pp; English.

XX CC New conjugates are disclosed which are of formula A-Z, in which: A is (1) a cyclosporin A analogue described in AW29087 or (2) an FK506 binding peptide inhibitor; and Z is a polypeptide comprising 5 or more contiguous residues of A-beta peptide. The compounds are novel chemical inducers of dimerization which are non-immunosuppressive and which are inhibitors of A-beta peptide aggregation and deposition in amyloid plaques. The adverse consequences of amyloid plaque formation can be prevented or ameliorated by sequestering the A-beta peptide in monomeric form with a conjugate which links the A-beta to cyclophilin or FKBP, therefore providing a mechanism to minimize the amount of free A-beta.

XX PA (SCIO-) SCIOS INC.
 XX PI Cordell B;
 XX DR WPI: 1999-357231/30.

XX PT Transgenic mice useful for studying compounds potentially useful in the treatment of Alzheimer's disease

XX Disclosure; Fig 3; 72pp; English.

PS

CC available for fibril formation and deposition. The compounds can be used
 CC for the treatment of Alzheimer's disease, multiple sclerosis and
 CC amyotrophic lateral sclerosis.

XX Sequence 42 AA;
 Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS Homo sapiens.
 Qy 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGALIGLMVGVVIA 42
 Db 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGALIGLMVGVVIA 42

RESULT 14

AAW99585
 ID AAW99585 standard; peptide: 42 AA.
 XX
 AC AAW99585;
 XX DT 22-JUN-1999 (first entry)
 DE Mutant aggregating amyloid-beta peptide.
 XX Aggregation; amyloid-beta peptide; fluorescent group; detection;
 KW diagnosis; Alzheimer's disease.
 XX Homo sapiens.
 OS Synthetic.
 XX PN W09908695-A1.
 XX PD 25-FEB-1999.
 XX PF 13-AUG-1998; 98WO-US16809.
 XX PR 14-AUG-1997; 97US-0055660.
 XX PA (RESC) UNIV CALIFORNIA.
 PT Garzon-Rodriguez W, Glabe C;
 XX DR WPI; 1999-190112/16.
 XX PT New fluorescent labeled amyloid A-beta Peptides
 PS Example 1; Page 21; 50pp; English.

XX This sequence corresponds to a mutant aggregating amyloid-beta peptide
 CC which can be covalently labelled with a fluorescent group. The detection
 CC or monitoring of an amyloid aggregate in a sample can be used to diagnose
 CC or detect a predisposition to Alzheimer's disease. The screening assays
 CC can be used to identify compounds for the treatment or amelioration of
 CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
 CC amyloid-beta peptide are also useful for exploring other aspects of
 CC amyloid structure.
 XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS Homo sapiens.
 Qy 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGALIGLMVGVVIA 42
 Db 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGALIGLMVGVVIA 42

RESULT 15

AAW92726
 ID AAW92726 standard; peptide: 42 AA.
 XX

AC AAW92726;
 XX 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #72.
 DE Tachykinin agonist; beta amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
 OS Homo sapiens.
 XX US5876948-A.
 XX PD 02-MAR-1999.
 XX PF 27-JUL-1991; 91US-0737371.
 XX PR 29-JUL-1991; 91US-0737371.
 XX PR 27-JUL-1990; 90US-0559173.
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX DR 1999-189630/16.
 XX PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX Disclosure; Column 41-42; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral hemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGATIGLMVGVVIA 42
 Db 1 DAEFRHDSGYEVHQKLVFFAEDGSNKGATIGLMVGVVIA 42

Search completed: April 21, 2003, 12:06:29
 Job time : 38 secs

RESULT 2
US-08-179-574-1
Sequence 1, Application US/08179574
GENERAL INFORMATION:
APPLICANT: Huntington Potter
TITLE OF INVENTION: Compounds and Methods for Inhibiting
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,574
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/819,361
FILING DATE: 13-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hanahan, Patricia
REGISTRATION NUMBER: 32-227
REFERENCE/DOCKET NUMBER: HU90-03A3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-08-179-574-1

Query Match 100.0% Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-08-347-144-1
Sequence 1, Application US/08347144
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: HORNEY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,144
FILING DATE: 08/08/97
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: AUBREY, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-347-144-1

Query Match 100.0% Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMGGVVIA 42
Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMGGVVIA 42

RESULT 4
US-08-462-859A-19
Sequence 19, Application US/08462859A
Patent No. 5654092
GENERAL INFORMATION:
APPLICANT: Jacobson, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: 5652092el Amyloid Precursor and Method of
Title of Invention: Using Same to Access Agents Which Down-Regulate Formation
Title of Invention: Of B-Amyloid Peptide
Number of Sequences: 19
Correspondence Address:
Addressee: American Cyanamid Company
City: Wayne
State: New Jersey
Country: United States
Zip: 07440-8426
Computer Readable Form:
Medium Type: Floppy disk
Computer: IBM PC compatible
Operating System: PC-DOS/MS-DOS
Software: PatentIn Release #1.0, Version #1.30
Current Application Data:

QY 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMGGVVIA 42
Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMGGVVIA 42

RESULT 4
US-08-462-859A-19
Sequence 1, Application US/08462859A
Patent No. 5589154
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: HORNEY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

Query Match Score 100.0%; Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

STREET: One Campus Drive
 CITY: Parsippany
 STATE: New Jersey
 COUNTRY: United States
 ZIP: 07054

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,247A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Barnhard, Elizabeth M.
 REGISTRATION NUMBER: 31,088

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-683-2158
 TELEFAX: 201-683-4117

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-464-247A-19

Query Match Score 100.0%; Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: United States
 ZIP: 07470-8426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,248A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Barnhard, Elizabeth M.
 REGISTRATION NUMBER: 31,088

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201)831-3246
 TELEFAX: (201)831-3305

RESULT 5
 US-08-123-659A-19

Sequence 19, Application US/08123659A
 ; Patent No. 565677

GENERAL INFORMATION:
 APPLICANT: Jacobsen, J. S.

TITLE OF INVENTION: 5656477el Amyloid Precursor and Method of Using Same to Access Agents Which Down-Regulate Formation of B-Amyloid Peptide

TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation of B-Amyloid Peptide

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 STREET: 163 Delaware Avenue, Suite 212
 CITY: Delmar
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 12054

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/123,659A
 FILING DATE: 20-SEP-1993
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Rosenblum, Anne M.
 REGISTRATION NUMBER: 30,419

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (518)475-0611
 TELEFAX: (518)475-0619

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-123-659A-19

Query Match Score 100.0%; Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

STREET: One Cyanamid Company
 CITY: Parsippany
 STATE: New Jersey
 COUNTRY: United States
 ZIP: 07054

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,248A
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Barnhard, Elizabeth M.
 REGISTRATION NUMBER: 31,088

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201)831-3246
 TELEFAX: (201)831-3305

RESULT 6
 US-08-464-247A-19

Sequence 19, Application US/08464247A
 ; Patent No. 563478

GENERAL INFORMATION:
 APPLICANT: Jacobsen, J. S.

TITLE OF INVENTION: 5693478el Amyloid Precursor and Method of Using Same to Access Agents Which Down-Regulate Formation of B-Amyloid Peptide

TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation of B-Amyloid Peptide

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 ADDRESS: American Cyanamid Company

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 100.0%; Score 217; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 0; Oligos 0;
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110-000010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

US-08-476-464A-1

Sequence 1, Application US/084,764,64A
Patent No. 5707821

GENERAL INFORMATION:
APPLICANT: RYDELL, RUSSELL E.
APPLICANT: DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2

ADDRESSEE: TOWNSEND & CREW LLP
STREET: TWO ENBARADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300

SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

RESULT 8

US-08-476-464A-1

Sequence 1, Application US/084,764,64A
Patent No. 5707821

GENERAL INFORMATION:
APPLICANT: RYDELL, RUSSELL E.
APPLICANT: DAPPEN, MICHAEL S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE
NUMBER OF SEQUENCES: 2

ADDRESSEE: TOWNSEND & CREW LLP
STREET: TWO ENBARADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)326-2400
TELEFAX: (415)576-0300

SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

RESULT 9

US-08-476-464A-1

Sequence 1, Application US/084,764,64A
Patent No. 5707821

GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994

RESULT 9

US-08-476-464A-1

Sequence 1, Application US/084,764,64A
Patent No. 5707821

GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994

CLASSIFICATION: 435
 PRIORITY APPLICATION DATA: PCT/JP94/00089
 FILING DATE: 24 JAN 1994
 APPLICATION NUMBER: 010132/1993
 FILING DATE: 25 JAN 1993
 APPLICATION NUMBER: 010035/1993
 FILING DATE: 05 FEB 1993
 APPLICATION NUMBER: 286385/1993
 FILING DATE: 16 NOV 1993
 APPLICATION NUMBER: 334773/1993
 FILING DATE: 28 DEC 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34-235
 REFERENCE/DOCKET NUMBER: 44631
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 TELEX: 200291 STRE
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 US-08-302-808-5

Query Match 100.0% Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42

RESULT 11
 US-08-268-348A-1

; Sequence 1, Application US/08268348A
 ; GENERAL INFORMATION:
 ; APPLICANT: Dobeli, Heinz
 ; APPLICANT: Draeger, Nicholas
 ; APPLICANT: Trottman, Gerda H
 ; APPLICANT: Jakob, Peter
 ; APPLICANT: Stuber, Dietrich
 ; TITLE OF INVENTION: Process for Producing Hydrophobic
 ; TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
 ; TITLE OF INVENTION: Producing Same
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hoffmann-La Roche Inc.
 ; STREET: 340 Kingsland Street
 ; CITY: Nutley
 ; COUNTRY: U.S.A.
 ; ZIP: 07110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/433,734
 ; FILING DATE: 03-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Muering, Ann M.
 ; REGISTRATION NUMBER: 33-977
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-305-1220
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 42 amino acids
 ; TYPE: amino acid
 ; TOPOLogy: linear
 ; MOLECULE TYPE: peptide

APPLICATION NUMBER: US/08/268348A
 FILING DATE: 29-JUN-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93110755.1
 FILING DATE: 06-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Parise, John P.
 REGISTRATION NUMBER: 34,403
 REFERENCE/DOCKET NUMBER: 4.105/157
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 235-6326
 TELEFAX: (201) 235-3500
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: N-terminal
 US-08-268-348A-1

Query Match 100.0% Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42

RESULT 12
 US-08-433-734-2

Query Match 100.0% Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42

RESULT 13
 US-08-433-734-3

Query Match 100.0% Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42

RESULT 14
 US-08-433-734-4

Query Match 100.0% Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42
 Db 1 DAEFRHDSGYEVHHQKLVEFAEDGSNKGATIGLMGGVIA 42

RESULT 15
 US-08-433-734-5

Query Match 100.0% Score 217; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4e-26;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-08-609-090-9
; Sequence 9, Application US/08609090

GENERAL INFORMATION:
; APPLICANT: HENSLY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-PEB-1996

ATTORNEY/AGENT INFORMATION:
; NAME: KRAUS, Eric J.
; REGISTRATION NUMBER: 36,190
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

Query Match 100 %; Score 217; DB 2; Length 42;
Best Local Similarity 100 %; Pred. No 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 14
US-07-137-371E-72
; Sequence 72, Application US/07737371E
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737, 371E
; FILING DATE: 29-JUL-1991

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154

INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-07-137-371E-72
Query Match 100 %; Score 217; DB 2; Length 42;
Best Local Similarity 100 %; Pred. No 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMVGGVVIA 42
Db 1 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMVGGVVIA 42

RESULT 15
US-08-422-333-4
; Sequence 4, Application US/08422333
; Patent No. 5912410

GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSCENDIC NON-HUMAN MAMMAL DISPLAYING THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; ZIP: 94043

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333
; FILING DATE: 13-APR-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Sheare, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; TELEFAX: (415) 968-2438
; INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-422-333-4

Query Match 100.0%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 4e-26;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLEFAEDVGSNKGAIIGLMYGGVIA 42
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DAEFRHDSGYEVHHQKLEFAEDVGSNKGAIIGLMYGGVIA 42
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: April 21, 2003, 12:08:07
Job time : 16 secs



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:07:50 ; Search time 22 Seconds

(without alignments)
 93.658 Million cell updates/sec

Perfect score: US-09-580-018-8

Sequence: 1 MDAEPRHDSC 10

Scoring table: Oligo Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1224

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SPTREMBL_211:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_invertebrate:*

5: sp_mammal:*

6: sp_mhc:*

7: sp_organelle:*

8: sp_phage:*

9: sp_plant:*

10: sp_rattus:*

11: sp_virus:*

12: sp_vertebrate:*

13: sp_unclassified:*

14: sp_virus:*

15: sp_bacteria:*

16: sp_archaea:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	8	13 Q9P69	Q9P69 gallus gallus
2	3	30.0	9	2 P72149	P72149 pseudomonas
3	3	30.0	10	6 Q9TU33	Q9TU33 canis familiaris
4	3	30.0	10	12 Q9JG8	Q9JG8 tt. virus. o
5	2	20.0	7	2 Q47477	Q47477 escherichia
6	2	20.0	7	4 Q15897	Q15897 homo sapiens
7	2	20.0	7	6 Q28742	Q28742 oryctolagus
8	2	20.0	7	8 Q9B866	Q9B866 spinacia ol
9	2	20.0	7	11 Q55184	Q55184 rattus norvegicus
10	2	20.0	8	2 Q68485	Q68485 klebsiella
11	2	20.0	8	2 Q9X3K1	Q9X3K1 prochlorococcus
12	2	20.0	8	2 Q9S6d5	Q9S6d5 escherichia
13	2	20.0	8	2 P72221	P72221 pseudomonas
14	2	20.0	8	2 Q9R7T2	Q9R7T2 escherichia
15	2	20.0	8	2 P83152	P83152 anabaena sp
16	2	20.0	8	2 Q9r3x0	Q9r3x0 planktothri

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SEQUENCES

SEQUENCE	RP	SEQUENCE	RP	SEQUENCE	RP
RX MEDLINE=2011685; PubMed=1918027;		RX MEDLINE=2011685; Barber D.L., Abersold R., Steyrer E., Shen X., Nimpf J.,		RX MEDLINE=2011685; Barber D.L., Abersold R., Steyrer E., Shen X., Nimpf J.,	
RA Stifani S.; Schneider W.J.;		RA Stifani S.; Barber D.L., Abersold R., Steyrer E., Shen X., Nimpf J.,		RA Stifani S.; Barber D.L., Abersold R., Steyrer E., Shen X., Nimpf J.,	
RT "The laying hen expresses two different low density lipoprotein receptor related proteins";		RT "The laying hen expresses two different low density lipoprotein receptor related proteins";		RT "The laying hen expresses two different low density lipoprotein receptor related proteins";	
RL J. Biol. Chem. 266:19079-19087(1991).		RL J. Biol. Chem. 266:19079-19087(1991).		RL J. Biol. Chem. 266:19079-19087(1991).	
FT NON_TER 1		FT NON_TER 1		FT NON_TER 1	
SQ SEQUENCE 8 AA; 88 MW; C00772DD865BAAA CRC64;		SQ SEQUENCE 8 AA; 846 MW; C00772DD865BAAA CRC64;		SQ SEQUENCE 8 AA; 846 MW; C00772DD865BAAA CRC64;	
Query Match 111		Query Match 111		Query Match 111	
Best Local Similarity 6.7e+05;		Best Local Similarity 6.7e+05;		Best Local Similarity 6.7e+05;	
Matches 3;		Matches 3;		Matches 3;	
Conservative 0;		Mismatches 0;		Mismatches 0;	
Indels 0;		Gaps 0;		Gaps 0;	

RESULT 1	PRELIMINARY;	PRT;	AA.
Q9P569			
ID Q9P569;			
AC Q9P669;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE Low density lipoprotein receptor-related protein (Fragment).			
OS Gallus gallus (Chicken).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OC Gallus.			
OX NCBI_TaxID=9031;			
[1]			
RN			
RX			
RA			
RA			
RT			
RT			
RT			
RL			
J. Biol. Chem. 266:19079-19087(1991).			
FT			
NON_TER			
SQ			
SEQUENCE 8 AA; 88 MW; C00772DD865BAAA CRC64;			
Query Match 111			
Best Local Similarity 6.7e+05;			
Matches 3;			
Conservative 0;			
Mismatches 0;			
Indels 0;			
Gaps 0;			

RESULT 2	PRELIMINARY;	PRT;	AA.
P72149			
ID P72149;			
AC P72149;			
DT 01-FEB-1997 (TREMBLrel. 02, Created)			

DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)	OC	Viruses; ssDNA viruses; unclassified ssDNA viruses.
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	OX	NCBI_TaxID=68887;
DE	Putative glucokinase (Fragment).	RN	[1]
GN		RP	SEQUENCE FROM N.A.
OS	Pseudomonas aeruginosa.	RC	STRAIN=TIV-SC232;
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	RX	MEDLINE=20251008; PubMed=10790123;
OC	Pseudomonas.	RA	Niel C., Saback F.L., Lampe E.
OX	NCBI_TaxID=287;	RT	"Coinfection with Multiple RT Virus Strains Belonging to Different Genotypes Is a Common Event in Brazilian Healthy Adults."
RN	[1]	RL	J Clin. Microbiol. 38:1926-1930(2000).
RP	SEQUENCE FROM N.A.	DR	EMBL; AF21653; AAP6689.1;
RC	STRAIN=PAOL;	SQ	SEQUENCE 10 AA; 1124 MW; 64IE2BD71B59CB CRC64;
RX	MEDLINE=96427344; PubMed=8830708;	Query Match	30.0%; Score 3; DB 12; Length 10;
RA	Sage A.E., Proctor W.D., Phibbs P.V.Jr.; "A two-component response regulator, gtrR, is required for glucose transport activity in <i>Pseudomonas aeruginosa</i> PAO1.", J. Bacteriol. 178:6064-6066(1996).	Best Local Similarity	100.0%; Pred. No. 4.3e+03;
RT		Matches	Mismatches 0; Indels 0; Gaps 0;
RL		QY	3 AEF 5
DR		Db	2 AEF 4
KW	Kinase.	RESULT 5	
FT	NON_TER 1 1 1	ID	Q47477 PRELIMINARY; PRT; 7 AA.
SEQUENCE	9 AA; 944 MW; C3071DDAA72DC6C6 CRC64;	AC	Q47477; Created
Query Match	30.0%; Score 3; DB 2; Length 9;	DT	01-NOV-1996 (TREMBLrel. 01, Created)
Best Local Similarity	100.0%; Pred. No. 6.7e+05; Mismatches 0; Indels 0; Gaps 0;	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
Matches	3; Conservative 0; Indels 0; Gaps 0;	DE	01-MAY-1999 (TREMBLrel. 10, Last annotation update)
QY	2 DAE 4	TPI	Tpi protein (Fragment).
Db	1 1	OS	Escherichia coli.
	6 DAE 8	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
RESULT 3		OC	Escherichia.
ID	Q9TU33	PRELIMINARY;	PRT; 10 AA.
AC	Q9TU33;		OC NCBI_TaxID=562;
DT	01-MAY-2000 (TREMBLrel. 13, Created)	RN	[1]
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	RP	SEQUENCE OF 7-7 PROM N.A.
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	RX	MEDLINE=85203917; PubMed=3158524;
DE	BRCA1 (Fragment).	RA	Hellinga H.W., Evans P.R.;
GN		RT	"Nucleotide sequence and high-level expression of the major
OS	Canis familiaris (Dog).	RT	Escherichia coli phosphofructokinase."
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RL	Eur. J. Biochem. 149:363-373(1985).
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	RN	[2]
OX	NCBI_TaxID=9615;	RP	SEQUENCE FROM N.A.
RN	[1]	RA	Evans P.;
RP	SEQUENCE FROM N.A.	RL	Submitted (Oct-1986) to the EMBL/GenBank/DDBJ databases.
RX	MEDLINE=854965; PubMed=10690375;	DR	EMBL; X02519; CAA26359.1; -
RA	Gray T.S., Yuzbasian-Gurcan V.;	FT	NON_TER 1
RT	"A single nucleotide (T->G) polymorphism within intron 23 of the canine BRCA1 gene."	SQ	SEQUENCE 7 AA; 773 MW; 7416D3DDDB1DB0 CRC64;
RT	canine Genet. 31:76-77(2000).;	Query Match	20.0%; Score 2; DB 2; Length 7;
RL	DR	Best Local Similarity	100.0%; Pred. No. 6.7e+05;
ANIMAL	Genet. 31:76-77(2000).;	Matches	Mismatches 0; Indels 0; Gaps 0;
DR	EMBL; AF159258; AAD56289.1; -.	QY	3 AE 4
NON_TER	1 1	Db	1 AE 2
FT	NON_TER 10 10	RESULT 6	
SEQUENCE	10 AA; 1164 MW; 2AB89C65BAAB01B3 CRC64;	ID	Q15897 PRELIMINARY; PRT; 7 AA.
Query Match	30.0%; Score 3; DB 6; Length 10;	AC	Q15897; Created
Best Local Similarity	100.0%; Pred. No. 4.3e+03; Mismatches 0; Indels 0; Gaps 0;	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
Matches	3; Conservative 0; Indels 0; Gaps 0;	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
QY	8 DSG 10	DE	(Clone XP011A) (Fragment).
Db	1 1	OS	Homo sapiens (Human).
	6 DSG 8	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
RESULT 4		OC	Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.
ID	Q9J1G8	PRELIMINARY;	PRT; 10 AA.
AC	Q9J1G8;		NCBI_TaxID=9606;
DT	01-OCT-2000 (TREMBLrel. 15, Created)	RN	SEQUENCE FROM N.A.
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	RP	
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	ORF.		
OS	TT virus.		

OC	Klebsiella	"Conserved organization in the cps gene clusters for expression of
OX	NCBI_TaxID=573;	Escherichia coli group 1 K antigens: relationship to the colanic acid
RN	(1)	biosynthesis loci and the cps genes from Klebsiella pneumoniae. ;
RP	SEQUENCE FROM N.A.	J. Bacteriol. 181:2307-2313(1999).
RC	STRAIN=K1;	RL
RX	MEDLINE=98287600; PubMed=9624504;	RT
RA	Centron D.; Roy P.H.;	RT
RT	"Characterization of the 6'-N-aminoglycoside acetyltransferase gene	RT
RT	aac(6')-Ig from the interon of a natural multiresistance plasmid. ;	RL
RL	Antimicrob Agents Chemother. 42:1506-1508 (1998).	DR
EMBL	AF047556; AAC55011; -.	FT
KW	Plasmid; Transferase.	NON_TER
FT	8	SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64;
SQ		Query Match 20.0%; Score 2; DB 2; Length 8;
		Best Local Similarity 100.0%; Pred. No. 6.7e+05;
		Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 AE 4	RESULT 13
Db	3 AE 4	P7221 PRELIMINARY; PRT; 8 AA.
		ID P7221
		AC P7221;
		DT 01-FEB-1997 (TREMBLrel. 02, Created)
		DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
		DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
		DE Alginate lyase (Fragment).
		GN ALY.
		OS Pseudomonas sp. (strain OS-ALG-9).
		OC Bacteria; Proteobacteria.
		NCBI_TAXID=86038;
		RN [1]
		RP SEQUENCE FROM N.A.
		RC STRAIN=OS-ALG-9;
		RA Fujiyama K.;
		RL Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
		RN [2]
		RP SEQUENCE FROM N.A.
		RC STRAIN=OS-ALG-9;
		RX MEDLINE=9339366; PubMed=8336113;
		RA Maki H.; Mori A.; Fujiyama K.; Kinoshita S.; Yoshida T.;
		RT "Cloning, sequence analysis and expression in Escherichia coli of a
		RT gene encoding an alginate lyase from Pseudomonas sp. OS-ALG-9.";
		RL J. Gen. Microbiol. 139:987-993 (1993).
		DR EMBL: D38469; BRA21704.1; -.
		KW Lyase.
		FT NON_TER 1
		FT NON_TER 1
		SQ SEQUENCE 8 AA; 799 MW; 10376865B72866D3 CRC64;
		Query Match 20.0%; Score 2; DB 2; Length 8;
		Best Local Similarity 100.0%; Pred. No. 6.7e+05;
		Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	9 SG 10	RESULT 14
Db	5 SG 6	Q9R7T2 PRELIMINARY; PRT; 8 AA.
		ID Q9R7T2
		AC Q9R7T2;
		DT 01-MAY-2000 (TREMBLrel. 13, Created)
		DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
		DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
		PUTATIVE IS30 transposase (Fragment).
		OS Escherichia coli.
		Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
		OC Escherichia
		OX NCBI_TaxID=562;
		RN [1]
		RP SEQUENCE FROM N.A.
		RC STRAIN=A295B;
		RX MEDLINE=39194747; PubMed=10094716;
		RA Rahn A., Drummond Smith J., Whitfield C.;
		RP SEQUENCE FROM N.A.
		RC STRAIN=K12;
		OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
		OC Escherichia.
		OX NCBI_TAXID=562;
		RN [1]
		RP SEQUENCE FROM N.A.
		RC STRAIN=K12;

RX MEDLINE=97061202; PubMed=8905232;
 RA Ohshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kaihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Take moto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
 to the 12.7-28.0 min Region on the Linkage Map.";
 RL DNA Res. 3:137-155(1996).;
 DR EMBL; D90705; BAA3531.0; -.

KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA: 964 MW: DF133BDD04B476A CRC64;

Query Match Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AE 4
 1 |
 Db 5 AE 6

RESULT 15

P83152 PRELIMINARY; PRT; 8 AA.
 ID P83152
 AC P83152;
 DT 01-MAR-2002 (TRMBrel. 20, Created)
 DT 01-MAR-2002 (TRMBrel. 20, Last sequence update)
 DT 01-MAR-2002 (TRMBrel. 20, Last annotation update)
 DE Allophycocyanin beta chain (Fragment).
 OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TAXID=29412;
 RN [1]
 RP SEQUENCE.

RA Apté S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.
 CC -|- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BIL PIGMENT-PROTEIN
 FROM THE PHOCOBILLIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM
 ABSORPTION AT APPROXIMATELY 650 TO 653 NANOMETERS.
 CC -|- SUBUNIT: HETEROODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -|- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.
 CC -|- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
 KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
 KW Thyylakoid; Membrane.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 788 MW: 87CDC1A05DDAB6DD CRC64;

Query Match Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DA 3
 1 |
 Db 3 DA 4

Search completed: April 21, 2003, 12:11:39
 Job time : 24 secs



Copyright (c) 1993 - 2003 Compugen Ltd.	GenCore version 5.1.4_p5_4578										
OM protein - protein search, using sw model											
Run on: April 21, 2003, 12:07:25 ; Search time 6.33333 Seconds (without alignments) 65.489 Million cell updates/sec											
Title: US-09-580-018-8											
Perfect score: 10											
Sequence: 1 MDAEFRHDSG 10											
Scoring table: OLIGO											
Searched: Gapop 60.0 , Gapext 60.0											
Word size : 0											
Total number of hits satisfying chosen parameters: 346											
Minimum DB seq length: 0											
Maximum DB seq length: 10											
Post-processing: Listing first 45 summaries											
Database : Swissprot_40:*											
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
SUMMARIES											
Result No.	Score	Query	Match	Length	DB ID	Description					
1	2	20.0	5	1	RE21_LITRU	P82071 litoria rub					
2	2	20.0	5	1	RE31_LITRU	P82072 litoria rub					
3	2	20.0	5	1	UXA4_CHLTR	P38005 chlamydia t					
4	2	20.0	6	1	FAR5_MONEX	P41966 moniezia ex					
5	2	20.0	6	1	TRPL_PSEPU	P36414 pseudomonas					
6	2	20.0	6	1	UN06_CLOPA	P81351 clostridium					
7	2	20.0	7	1	FARI_ASCSDU	P31889 ascaris suu					
8	2	20.0	7	1	UF03_MOUSE	P38641 mus musculu					
9	2	20.0	8	1	ALI7_CARNA	P81820 carcinus ma					
10	2	20.0	8	1	CKKN_MACFU	P30369 macropus eu					
11	2	20.0	8	1	CPD1_LENTFA	P13269 enterococcus					
12	2	20.0	8	1	GLOR_HUMAN	P02729 homo sapien					
13	2	20.0	8	1	LCK4_LEIDMA	P21143 leucophasea					
14	2	20.0	8	1	LCK5_LEIDMA	P19987 leucophasea					
15	2	20.0	8	1	ORMY_ORCULI	P82455 orconectes					
16	2	20.0	8	1	PPK3_PERAM	P82618 periplaneta					
17	2	20.0	8	1	UC26_MAIZZE	P80632 zea mays (m					
18	2	20.0	8	1	VGIG_HSV2B	P01780 herpes simp					
19	2	20.0	9	1	CXOE_THIOP	P80975 thunnus obe					
20	2	20.0	9	1	DSIP_RABIT	P01158 orctolagus					
21	2	20.0	9	1	FA55_ASCSU	P43170 ascaris suu					
22	2	20.0	9	1	FAR6_CALVO	P41861 calliphora					
23	2	20.0	9	1	FIB2_MACFU	P19345 macaca fusc					
24	2	20.0	9	1	FIBB_PAPAN	P19344 patio anubi					
25	2	20.0	9	1	IPYR_RHOVI	P82992 rhodopseudo					
26	2	20.0	9	1	MOSF_CLYJA	P19853 clypeaster					
27	2	20.0	9	1	MOSH_CLYJA	P19852 clypeaster					
28	2	20.0	9	1	NEU1_CAVPO	P34966 cavia porce					
29	2	20.0	9	1	NEUX_HUMAN	P04277 homo sapien					
30	2	20.0	9	1	OXYT_OCTVU	P80027 octopus vul					
31	2	20.0	9	1	TKL1_LOCM1	P16223 locusta mig					
32	2	20.0	9	1	TRP4_LEIDMA	P81736 leucophasea					
33	2	20.0	9	1	XYL1_STRSO	P19149 streptomyce					
ALIGNMENTS											
RESULT 1											
RE21_LITRU	ID	RE21_LITRU	STANDARD;	PRT;	5 AA.						
AC	P82071;										
DT	15-JUN-2002 (Rel. 4.1, Created)										
DT	15-JUN-2002 (Rel. 4.1, Last sequence update)										
DT	15-JUN-2002 (Rel. 4.1, Last annotation update)										
DE	Rubellidin 2.1.										
OS	Litoria rubella (Desert tree frog).										
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrichia; Anura; Neobatrachia; Bufonoidea; Hyliidae;										
OX	NCBI_TaxID:104895;										
RN	[1]										
RP	SEQUENCE, AND MASS SPECTROMETRY.										
RC	TISSUE=Skin Secretion;										
RA	Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,										
RA	Tyler M.J., Wallace J.C.;										
RT	"The structure of new peptides from the Australian red tree frog of evolutionary trends of amphibians."										
RT	Aust. J. Chem. 49: 955-963 (1996).										
RL	-1 - FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBOTIC ACTIVITY.										
CC	--! TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.										
CC	--! MASS SPECTROMETRY: MW=6265; METHOD=PAB.										
KW	Amphibian skin.										
SQ	SEQUENCE 5 AA: 626 MW: 6DD9C9CB10300000 CRC64;										
Query Match	20.0%; Score 2; DB 1; Length 5;										
Best Local Similarity	100.0%; Pred. No. 1.1e+05;										
Matches	2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;										
QY	4 EF 5										
Db	1 EF 3										
RESULT 2											
RE31_LITRU	ID	RE31_LITRU	STANDARD;	PRT;	5 AA.						
AC	P82072;										
DT	15-JUN-2002 (Rel. 4.1, Created)										
DT	15-JUN-2002 (Rel. 4.1, Last sequence update)										
DT	15-JUN-2002 (Rel. 4.1, Last annotation update)										
DE	Rubellidin 3.1.										
OS	Litoria rubella (Desert tree frog).										
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrichia; Anura; Neobatrachia; Bufonoidea; Hyliidae;										
OC	Pelodryadinae; Litoria.										
OX	NCBI_TaxID:104895;										
RN	[1]										
RP	SEQUENCE, AND MASS SPECTROMETRY.										
RC	TISSUE=Skin Secretion;										
RA	Steinborner S.T., Wallace J.C.,										
RA	Tyler M.J., Wallace J.C.,										

RT "The structure of new peptides from the Australin red tree frog of evolutionary trends of amphibians.";
 RT Aust. J. Chem. 19;955-963(1996).
 RL -!- ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 AMIDATION.
 SQ SEQUENCE 5 AA; 655 MW; 71A9C9CB10300000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 20.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 20.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 20.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 URA4_CHLTR STANDARD; PRT; 5 AA.

ID URA4_CHLTR
 AC P38005; 30, Created
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 OS Unknown protein from 2D-page from elementary body (Fragment).
 OC Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydida.
 OC NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PGL1 C1S;
 RX MEDLINE=89335806; PubMed=2503057;
 RA Berry L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of *Pseudomonas putida*.";
 RL Biochimie 71:521-531(1989).

CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPB GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL PHOSPHATE), TRII BINDS UPSTREAM OF THE TRPB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

Query Match 20.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 20.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 20.0%; Score 2; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 FARP_MONEX STANDARD; PRT; 6 AA.

ID FARP_MONEX
 AC P41966; 32, Created
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide GNFRF-amide.
 OS Moniezia expansa (Sheep tapeworm).
 OC Eularysta; Netozoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidea; Anoplocephalidae; Moniezia.
 OX NCBI_TaxID=28841; [1]
 RP SEQUENCE. MEDLINE=93312289; PubMed=8323531;

RX Maule A.G., Shaw C., Halton D.W., Thim L.; "GNFRamide: a novel FMRFamide-immunoreactive peptide isolated from the sheep tapeworm, *Moniezia expansa*"; Biochem. Biophys. Res. Commun. 193:1054-1060(1993).

RESULT 6
 UN06_CLOPA STANDARD; PRT; 6 AA.

ID UN06_CLOPA
 AC P81351;
 DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 6 from 2D-page (Fragment).
 OS Clostridium Pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium; NCBI_TaxID=1501;
 OX [1]
 RN RP
 SEQUENCE:
 STRAIN=W5;
 RC MEDLINE=98299870; PubMed=96299918;
 RX RA Fjengsrød R.; Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 sequencing analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -1 - MISCELLANEOUS : ON THE 2D GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
 CC NON_TER 6 6
 FT SEQUENCE 6 AA: 657 MW: 605B1D1A45A8000 CRC64;
 SQ

Query Match Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AE 4	3 AE 4	20.0%	Score 2;	DB 1;	Length 7;
Db 4 AE 5	4 AE 5	Best Local Similarity 100.0%;	Pred. No. 1.1e+05;	Mismatches 0;	Indels 0; Gaps 0;

RESULT 7
 FARI_ASCTU
 ID FARI_ASCTU
 AC P31889;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuropeptide AF1.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nemataoda; Chromadorea; Ascaridoidea;
 OC Ascaridae; Ascaris.
 OX [1]
 RN RP
 SEQUENCE:
 MEDLINE=90180465; PubMed=2627377;
 RA Cowden C., Stretton A.O.W., Davis, R.E.
 RT "AF1, a sequenced bioactive neuropeptide isolated from the nematode
Ascaris suum.";
 RT Neuron 2:1455-1473(1989).
 CC -1 - FUNCTION: POTENT MODULATOR OF INHIBITORY MOTORNEURONS. REDUCES THE
 INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
 CELLS.
 CC -1 - TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
 GLANDIA PARTICULARLY IN THE ANTERIOR REGIONS.
 CC -1 - SIMILARITY: BELONGS TO THE FARF (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7
 SQ AMIDATION.
 SEQUENCE 7 AA: 953 MW: 69d40059B144350 CRC64;

Query Match Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EF 5	4 EF 5	20.0%	Score 2;	DB 1;	Length 8;
Db 3 EF 4	3 EF 4	Best Local Similarity 100.0%;	Pred. No. 1.1e+05;	Mismatches 0;	Indels 0; Gaps 0;

RESULT 8
 UF03_MOUSE
 ID UF03_MOUSE
 AC P31641;
 DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of Fibroblasts (P36) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP
 SEQUENCE:
 RC TISSUE=Fibroblast;
 RX MEDLINE=9009907; PubMed=7521108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT Separation and sequencing of familiar and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -1 - MISCELLANEOUS : ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA: 842 MW: 6AA72BLDDB1B1180 CRC64;

Query Match Score 20.0%; Score 2;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AE 4	3 AE 4	20.0%	Score 2;	DB 1;	Length 7;
Db 4 AE 5	4 AE 5	Best Local Similarity 100.0%;	Pred. No. 1.1e+05;	Mismatches 0;	Indels 0; Gaps 0;

RESULT 9
 AL17_CARMA
 ID AL17_CARMA
 AC P81830;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 17.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Pancrustacea; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP
 SEQUENCE:
 RC TISSUE=Cerebral ganglion and Thoracic ganglion;
 RX MEDLINE=91121193; PubMed=9461195;
 RA Duwe H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 allatoxstatin superfamily in the shore crab *Carcinus maenas*."
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1 - FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1 - SIMILARITY: BELONGS TO THE ALLATOXSTATIN FAMILY.
 KW Neuropeptide; Amidation (POTENTIAL).
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA: 858 MW: C82879D5AB46D865 CRC64;

Query Match Score 20.0%; Score 2;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SG 10	9 SG 10	20.0%	Score 2;	DB 1;	Length 8;
Db 1 SG 2	1 SG 2	Best Local Similarity 100.0%;	Pred. No. 1.1e+05;	Mismatches 0;	Indels 0; Gaps 0;

RESULT 10
 CCKN_MACEU
 ID CCKN_MACEU
 AC P30365;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Cholecystokinin (CCK). GN Macropterus eugenii (Tamarar wallaby), and OS Dasyurus viverrinus (Southeastern quoll). OS Mammalia; Metazoa; Chorata; Craniata; Vertebrata; Euteleostomi; OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9315, 9279; [1]	DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DE Urine glycopeptide. OS Homo sapiens (Human). OC Metazoa; Eutheria; Primates; Catarrhini; Hominidae; Homo. OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TAXID=9606; RN [1] RP SEQUENCE.	DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DE Urine glycopeptide. RT "Identification in urine of a low-molecular-weight highly polar glycopeptide containing cysteinyl-galactose."; RL Biochem. J. 123:25P-25P(1971). CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A SIMILAR STRUCTURE HAS ALSO BEEN FOUND. CC DR PIR; A03188; XGHBEU. KW Glycoprotein. FT CARBOHYD 1 S-LINKED (GAL.). SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1E1E CRC64;
DR Interf1; PQ0012; P00012. DR IPR01651; Gastrin. DR PROSITE; PS00239; GASTRIN; 1. KW Amidation; Sulivation; Hormone. FT Amidation, 2; Sulfation, 2 MOD_RES 8 8 AMIDATION, SEQUENCE 8 AA; 1064 MW; DDCAA8378768B5A CRC64;	Query Match 20.0%; Score 2; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 MD 2 Db 6 MD 7	Query Match 20.0%; Score 2; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 7 HD 8 Db 5 HD 6
DR PIR; A43001; A43001. DR IPR01651; Gastrin. DR PROSITE; PS00239; GASTRIN; 1. KW Amidation; Sulivation; Hormone. FT Amidation, 2; Sulfation, 2 MOD_RES 8 8 AMIDATION, SEQUENCE 8 AA; 1064 MW; DDCAA8378768B5A CRC64;	Query Match 20.0%; Score 2; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 MD 2 Db 6 MD 7	Query Match 20.0%; Score 2; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 7 HD 8 Db 5 HD 6
DR IPR01651; Gastrin. DR PROSITE; PS00239; GASTRIN; 1. KW Amidation; Sulivation; Hormone. FT Amidation, 2; Sulfation, 2 MOD_RES 8 8 AMIDATION, SEQUENCE 8 AA; 1064 MW; DDCAA8378768B5A CRC64;	Query Match 20.0%; Score 2; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 MD 2 Db 6 MD 7	Query Match 20.0%; Score 2; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 7 HD 8 Db 5 HD 6
RESULT 11 CPD1_ENTFA ID CPD1_ENTFA AC P13265 DT 01-JAN-1990 (Rel. 13, Created) DT 01-JAN-1990 (Rel. 13, Last sequence update) DT 01-FEB-1991 (Rel. 17, Last annotation update) DE CPD1 OS Enterococcus faecalis (Streptococcus faecalis). OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus. NCBI_TAXID=1351; OX [1]	STANDARD; PRT; 8 AA.	STANDARD; PRT; 8 AA.
RN SEQUENCE. RX MEDLINE=85040388; PubMed=6436978; RA Craig R.A., Clewell D.B.; RA Mori M., Sagami Y., Isogai A., Fujino M., Kitada C., RA "Isolation and structure of bacterial sex pheromone, CPD1." RL Science 226:84-85(1984). CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE BACTERIOCIN PLASMID PPD1. KW Pheromone. SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;	STANDARD; PRT; 8 AA.	STANDARD; PRT; 8 AA.
Query Match 20.0%; Score 2; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 9 SG 10 Db 7 SG 8	Query Match 20.0%; Score 2; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 9 SG 10 Db 7 SG 8	Query Match 20.0%; Score 2; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 9 SG 10 Db 7 SG 8
RESULT 12 GLUR_HUMAN ID GLUR_HUMAN AC P02729;	PRT; 8 AA.	PRT; 8 AA.
RESULT 14 LCK5_LEUMA ID LCK5_LEUMA	STANDARD; PRT; 8 AA.	STANDARD; PRT; 8 AA.

Search completed: April 21, 2003, 12:10:27
 Job time : 8.33333 secs

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AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Leucokinins V (L-V).
OS Leucophaea maderae (Madeira cockroach)
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthoptera; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TAXID=6988;
RN [1]
RN RP
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=8/052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.:
RT "Isolation, primary structure, and synthesis of leucokinins V and VI:
  myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
  ACTIVITY OF COCKROACH PROTEIN (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR; JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SEQUENCE 8 AA; 784 MW; 736365A5B9C65B8 CRC64;
SQ Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SG 10
      |||
Db 2 SG 3

RESULT 15
ORMY_ORCLI
ID ORMY_ORCLI STANDARD; PRT; 8 AA.
AC P82455;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orconectin (OMT).
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Astacidea; Astacoidea; Cambaridae; Orconectes.
OX NCBI_TAXID=28379;
RN [1]
RN RP
RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Hindgut;
RX MEDLINE=20411310; PubMed=10952880;
RA Dirksen H., Burdzik S., Sauter A., Keller R.:
RT "Two orcokinins and the novel octapeptide orconomyotropin in the hindgut
  of the crayfish Orconectes limosus: identified myostimulatory
  neuropeptides originating together in neurons of the terminal
  abdominal ganglion."
RT J. Exp. Biol. 203: 2807-2818 (2000).
CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
  AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
  BY ABDOMINAL GANGLIONIC NEURONS.
CC -1- MASS SPECTROMETRY: MW=904 .8; METHOD=FAB.
KW Amidation; Neuropeptide.
FT MOD_RES 8 8 AMIDATION.
SEQUENCE 8 AA; 905 MW; 872861B1A9CDDAA9 CRC64;
SQ Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DA 3
      ||
Db 2 DA 3

```



4 protein - protein search, using sw model																	
run on:		April 21, 2003, 12:08:10 ; Search time 11.6667 Seconds (without alignments) 82.401 Million cell updates/sec															
little:	US-09-580-018-8																
percent score:	10																
sequence:	1 MDAEFFRHDSG 10																
scoring table: OLIGO Gapext 60.0 , Gapext 60.0																	
searched: 283224 seqs, 96134422 residues																	
word size :	0																
minimum DB seq length: 0																	
maximum DB seq length: 10																	
total number of hits satisfying chosen parameters: 1100																	
post-processing: Listing first 45 summaries																	
database :	PIR_73:*																
1:	pir1:*																
2:	pir2:*																
3:	pir3:*																
4:	pir4:*																
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.																	
SUMMARIES																	
8																	
result No.	Score	Query Match Length	DB ID	Description													
1	3	30.0	5 2	A26830													
2	3	30.0	7 2	PT0283													
3	3	30.0	8 2	S78036													
4	3	30.0	9 2	PL0139													
5	3	30.0	10 2	PH0900													
6	2	20.0	3 3	PT0571													
7	2	20.0	4 2	I51049													
8	2	20.0	4 2	PT0633													
9	2	20.0	4 2	PT0711													
10	2	20.0	4 2	PT0698													
11	2	20.0	4 2	PT0677													
12	2	20.0	4 2	PT0706													
13	2	20.0	4 2	PT0675													
14	2	20.0	4 2	PT0566													
15	2	20.0	5 2	B25216													
16	2	20.0	5 2	C23751													
17	2	20.0	5 2	A41225													
18	2	20.0	5 2	B41225													
19	2	20.0	5 2	B31836													
20	2	20.0	5 2	D60274													
21	2	20.0	5 2	B37988													
22	2	20.0	5 2	J44692													
23	2	20.0	5 2	JT0520													
24	2	20.0	5 2	D44823													
25	2	20.0	5 2	PT0596													
26	2	20.0	5 2	PT0513													
27	2	20.0	5 2	PT0600													
28	2	20.0	5 2	PT0669													
29	2	20.0	5 2	PT0669													

S78036 ribosomal protein Yms-B, mitochondrial - yeast (*Saccharomyces cerevisiae*) (fragment)
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
 C;Accession: S78036
 R;Kitagawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittmaier, J. Biochem. 245, 449-456, 1997
 A;Title: Identification and characterization of the genes for mitochondrial ribosomal proteins
 A;Reference number: S78018; PMID:97296414; PMID:9151978
 A;Accession: S78036
 A;Molecule type: protein
 A;Residues: 1-8 <KTR>
 C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match	30.0%	Score 3;	DB 2;	Length 8;
Best Local Similarity	100.0%	Pred. No. 2.	2.e+05;	
Matches 3;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 8 DSG 10
 Db 6 DSG 8

RESULT 4
 PL0139 carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - *Pseudomonas carboxydoflava* (fr)
 C;Species: *Pseudomonas carboxydoflava*
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
 R;Kraut, M.; Hugendieck, I.; Hervig, S.; Meyer, O.
 Arch. Microbiol. 152, 335-341, 1989
 A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria
 A;Accession: PL0139
 A;Molecule type: protein
 A;Residues: 1-9 <KR>
 A;Note: 2-Met is also found
 C;Comment: Cardon-monoxide dehydrogenase consists of three polypeptide chains: large, medium and small
 C;Keywords: oxidoreductase

Query Match	30.0%	Score 3;	DB 2;	Length 9;
Best Local Similarity	100.0%	Pred. No. 2.	2.e+05;	
Matches 3;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 2 DAE 4
 Db 7 DAE 9

RESULT 5
 PH0900 T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0900
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbergk, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalitis
 A;Reference number: PH0891; PMID:92078837; PMID:1836012
 A;Accession: PH0900
 A;Molecule type: mRNA
 A;Residues: 1-10 <GOL>
 A;Experimental source: myelin basic protein-immunized T-cell

Query Match	30.0%	Score 3;	DB 2;	Length 10;
Best Local Similarity	100.0%	Pred. No. 1.	3.e+03;	
Matches 3;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 8 DSG 10
 Db 5 DSG 7

RESULT 6
 PT0571 T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: PT0571
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A;Reference number: PT0509; PMID:91277601; PMID:1711558
 A;Accession: PT0571
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-3 <FEE>
 A;Experimental source: day 19 fetal thymus, strain BALB/C
 C;Keywords: T-cell receptor

Query Match	20.0%	Score 2;	DB 3;	Length 3;
Best Local Similarity	100.0%	Pred. No. 2.	8.e+05;	
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 9 SG 10
 Db 2 SG 3

RESULT 7
 T51049 metallothionein-A - rainbow trout (fragment)
 C;Species: *Oncorhynchus mykiss* (rainbow trout)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C;Accession: T51049
 R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
 Eur. J. Biochem. 230, 344-349, 1995
 A;Title: Structural and functional analysis of the rainbow trout (*Oncorhynchus mykiss*)
 A;Reference number: 151049; PMID:95224545; PMID:7601121
 A;Accession: T51049
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-4
 A;Cross references: EMBL:X80181; PIDN:91019799; PIDN:CAA564661; PID:94379328

Query Match	20.0%	Score 2;	DB 2;	Length 4;
Best Local Similarity	100.0%	Pred. No. 2.	8.e+05;	
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 MD 2
 Db 1 MD 2

RESULT 8
 PT0633 T-cell receptor beta chain V-D-J region (120-2C) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0633
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A;Reference number: PT0509; PMID:91277601; PMID:1711558
 A;Accession: PT0633
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: newborn thymus, strain BALB/C
 C;Keywords: T-cell receptor

Query Match	20.0%	Score 2;	DB 2;	Length 4;
Best Local Similarity	100.0%	Pred. No. 2.	8.e+05;	
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 9 SG 10
Db 1 |
Db 2 SG 3

RESULT 9
PT011 T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Accession: PT0509; MUID:91277601; PMID:1711558
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE1>
A;Experimental source: newborn thymus, strain BALB/c, 120-2J
A;Accession: PT0674
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A;Accession: PT0678
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A;Accession: PT0700
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE4>
A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A;Accession: PT0711
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE5>
A;Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
PT0698 T-cell receptor beta chain V-D-J region (126-1AH) - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Accession: PT0546; PT0638; PT0583
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE6>
A;Accession: PT0698
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE7>
A;Experimental source: newborn thymus, strain BALB/c, 126-1AH
A;Accession: PT0583
A;Status: translation not shown

Query Match 20.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
PT0675

T-cell receptor beta chain V-D-J region (140-1AC) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0675
 R;Feeney, A.J.
 J;Exp_Med_174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0675
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/C
 C;Keywords: T-cell receptor

Qy	9	SG	10
Db	2	SG	3

Query Match Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 PR0566
 T-cell receptor beta chain V-D-J region (141-1CH) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0566
 R;Feeney, A.J.
 J;Exp_Med_174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0566
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FEE>
 A;Experimental source: day 19 fetal thymus, strain BALB/C
 C;Keywords: T-cell receptor

Qy	9	SG	10
Db	2	SG	3

Query Match Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
 A32516
 cholecystokinin-5 - dog
 N;Alternate names: cck-5
 C;Species: Canis lupus familiaris (dog)
 C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
 C;Accession: A32516
 R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
 Am. J. Physiol. 252, G272-G275, 1987
 A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intestines
 A;Reference number: A32516; MUID:87153871; PMID:3826354
 A;Accession: A32516
 A;Molecule type: protein
 A;Residues: 1-5 <SHI>
 C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto-

C;Superfamily: gastrin
 C;Keywords: amidated carboxyl end; neuropeptide
 F;Modified site: amidated carboxyl end (Phe) #status experimental
 Query Match Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gencore version 5.1.4-p5 4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:12:26 ; Search time 28 Seconds

(without alignments)
73.588 Million cell updates/secTitle: US-09-580-018-5
Perfect score: 10
Sequence: 1 EVKMDAEFRH 10

Scoring table: Oligo

Gapext 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 5

Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database :	SPTRMBL_21:*
	1: sp_archaea:*
	2: sp_bacteria:*
	3: sp_fungi:*
	4: sp_human:*
	5: sp_invertebrate:*
	6: sp_mammal:*
	7: sp_mhc:*
	8: sp_organelle:*
	9: sp_phage:*
	10: sp_plant:*
	11: sp_rhodent:*
	12: sp_virus:*
	13: sp_vertebrate:*
	14: sp_unclassified:*
	15: sp_virus:*
	16: sp_bacteriopl:*
	17: sp_archaea:*

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1	10.0	5	2	P83073	P83073 bacillus ce
2	1	10.0	5	10	Q99007	Q99007 hordeum ce
3	1	10.0	5	13	P83308	P83308 gallus gall
4	1	10.0	6	10	P82181	P82181 spinacia ol
5	1	10.0	6	10	P82541	P82541 spinacia ol
6	1	10.0	6	10	P82182	P82182 spinacia ol

ALIGNMENTS

RESULT 1	P83073	ID	P83308	PRELIMINARY;	PRT;	5 AA.
	ID P83073	AC P83073;	AC P83308;			
	DT 01-OCT-2001	(TREMBLrel. 18, Created)	DT 01-JUN-2002	(TREMBLrel. 21, Created)		
			DT 01-JUN-2002	(TREMBLrel. 21, Last sequence update)		

DT 01-OCT-2001	(TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001	(TREMBLrel. 18, Last annotation update)
DE 88 kDa protein (Fragment).	
OS Bacillus cereus.	
OC Bacteria; Firmicutes; Bacillales/Clostridiium group; Bacillales;	
OC Bacillaceae; Bacillus.	
OX NCBI_TaxID=1396;	
RN [1]	
RP	
RC STRAIN=NCIMB 11796;	
RA Browne N. Dowds B.C.A.;	
RL Submitted (JUL-2001) to the SWISS-PROT data bank.	
FT NON_TER 5	
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;	
SEQUENCE.	
Query Match 10.0%; Score 1; DB 2; Length 5;	
Best Local Similarity 100.0%; Pred. No. 6.7e+05;	
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 4 M 4	
Db 1 M 1	

RESULT 2		
Q99007		
ID 099007	PRELIMINARY;	
AC 099007;	PRT;	5 AA.
DT 01-NOV-1996	(TREMBLrel. 01, Created)	
DT 01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DE 01-NOV-1998	(TREMBLrel. 08, Last annotation update)	
GN Alpha-amylase (EC 3.2.1.1) (Fragment).		
GN AMY1.		
OS Hordeum vulgare (Barley).		
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pooidae;		
OC Triticeae; Hordeum.		
OX NCBI_TaxID=4513;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;		
RX MEDLINE=91329704; PubMed=1831055;		
RA Jacobsen J.V., Close T.J.;		
RT "Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers." RT Plant Mol. Biol. 16:713-721(1991).		
RT Plant Mol. Biol. 16:713-721(1991).		
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.		
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.		
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.		
CC DR EMBL; X54643; CAA38455.1; -		
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;		
KW Calcium; Multigene family.		
FT NON_TER 5		
SQ SEQUENCE 5 AA; 600 MW; 61E334DD6F00000 CRC64;		
BARLEY.		
Query Match 10.0%; Score 1; DB 10; Length 5;		
Best Local Similarity 100.0%; Pred. No. 6.7e+05;		
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 4 M 4		
Db 1 M 1		

RESULT 5
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE FMRFamide-like neuropeptide (LPLRF-amide).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TAXID=9031;
 RN [1]
 RP SEQUENCE, NND SYNTHESIS.
 RC TISSUE=BRAIN;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R., Jr., Shirely J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 antibodies to FMRFamide.";
 RL Nature 305:328-330(1983).
 CC -|- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA: 645 MW: 69D407367400000 CRC64;
 Query Match Score 10.0%; Score 1; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 R 9
 Db 4 R 4
 RESULT 4
 ID P82181 PRELIMINARY; PRT; 6 AA.
 AC P82181;
 DR 01-JUN-2000 (TREMBLrel. 14, Created)
 DR 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DR 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
 OS Spinacia olereacea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermato phyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TAXID=3562;
 RN [1]
 RP SEQUENCE, STRAIN=CV, ALWARO; TISSUE=LEAF.
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 the 50 S subunit of an organelle ribosome (chloroplast)." ;
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -|- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR01790; Ribosomal L10.
 DR InterPro: IPR02363; Ribosomal L10eub.
 DR Pfam: PF00466; Ribosomal L10; PARTIAL.
 DR PROSITE: PS01109; Ribosomal L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 SQ SEQUENCE 6 AA: 6321B415B05DB000 CRC64;
 Qy 9 R 9
 Db 2 R 2
 RESULT 6
 ID P82182 PRELIMINARY; PRT; 6 AA.
 AC P82182;
 DR 01-JUN-2000 (TREMBLrel. 14, Created)
 DR 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DR 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
 OS Spinacia olereacea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermato phyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TAXID=3562;
 RN [1]
 RP SEQUENCE, STRAIN=CV, ALWARO; TISSUE=LEAF;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 the 50 S subunit of an organelle ribosome (chloroplast)." ;
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.

CC !- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001780; Ribosomal_L10.
DR InterPro; IPR002363; Ribosomal_L10ub.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
DR Ribosomal protein, Chloroplast; rRNA-binding.
FT NON_TER 6
SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
Query Match 10.0%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; P-reqd. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 A 6
Db 1 A 1

Search completed: April 21, 2003, 12:15:07
Job time : 28 secs



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:11:46 ; Search time 10 Seconds
(without alignments)
41.476 Million cell updates/sec

{ Title: US-09-580-018-5
-Perfect score: 10
Sequence: 1 EVKMDAEFRH 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 5
Maximum DB seq length: 6

Post-processing: Listing first 45 summaries

Database : Swissprot_40; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2	20.0	5	1	RE21_LITRU	P82071	litoria rub
2	2	20.0	5	1	RE31_LITRU	P82072	litoria rub
3	2	20.0	5	1	UC22_NAIVE	P80628	zea mays
4	2	20.0	6	1	FARP_NONEX	P41966	moniezia ex
5	2	20.0	6	1	UN06_CLOPA	P81351	clostridium
6	1	10.0	5	1	AL14_CARMA	P81817	carcinus ma
7	1	10.0	5	1	BIOA_CITER	P13071	citrobacter
8	1	10.0	5	1	BIOB_LITFR	P12997	citrobacter
9	1	10.0	5	1	BPP7_BOTIN	P30425	bothrops in
10	1	10.0	5	1	E103_LITRU	P82099	litoria rub
11	1	10.0	5	1	E104_LITRU	P82100	litoria rub
12	1	10.0	5	1	FARP_BTTR	P41853	artroposthi
13	1	10.0	5	1	PAP2_PARMA	P81864	paracardiorus
14	1	10.0	5	1	PRCT_FERAM	P01373	periplaneta
15	1	10.0	5	1	RE11_LITRU	P82070	litoria rub
16	1	10.0	5	1	RE32_LITRU	P82073	litoria rub
17	1	10.0	5	1	SUGA_ACHDO	P19991	acheta dome
18	1	10.0	5	1	TPI3_ANFA	P54714	canis famili
19	1	10.0	5	1	TRM3_ECOLI	P13973	escherichia
20	1	10.0	5	1	UF01_MOUSE	P38639	mus musculu
21	1	10.0	5	1	UXA4_EHLTR	P38005	chlamydia t
22	1	10.0	6	1	ACPH_RABBIT	P25154	oryctolagus
23	1	10.0	6	1	ASP2_IACSN	P89655	lactobacill
24	1	10.0	6	1	CIP1_NYTED	P13736	mytilus ediu
25	1	10.0	6	1	CIP2_NYTED	P13737	mytilus ediu
26	1	10.0	6	1	E101_LITRU	P82096	litoria rub
27	1	10.0	6	1	LOKL_LOCMI	P41491	locusta mig
28	1	10.0	6	1	OVM_LEPD	P42985	leptinotars
29	1	10.0	6	1	TMOF_SARB	P41495	sarcophaga
30	1	10.0	6	1	TRPL_PSEPU	P36414	pseudomonas
31	1	10.0	6	1	VP19_HSVIK	P22210	herpes simp
32	0	0.0	5	1	PSK_DAUCA	P58261	daucus caro

RESULT 1
RE21_LITRU STANDARD PRT; 5 AA.
ID P82071; (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodryadinae; Litoria;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963 (1996).
CC !- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC !- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC !- MASS SPECTROMETRY: MW=626; METHOD=FAB.
SQ SEQUENCE 5 AA; 6DD9C9CB10300000 CRC64;
Query Match Score 20.0%; Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
RE31_LITRU STANDARD PRT; 5 AA.
ID P82072; (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodryadinae; Litoria;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963 (1996).
CC !- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC !- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC !- MASS SPECTROMETRY: MW=655; METHOD=FAB.
SQ SEQUENCE 5 AA; 656 MW; 71AS9C9CB10300000 CRC64;
Query Match Score 20.0%; Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 7 EF 8 Db 2 EF 3	Qy 8 FR 9 Db 4 FR 5	Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 3			
UC22_MAIZE ID UC22_MAIZE STANDARD; PRT; 5 AA. AC P80638; DT 01-OCT-1996 (Rel. 34, Created) DT 15-JUL-1996 (Rel. 38, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DB Unknown protein from 2D-page of etiolated coleoptile (Spot 474) DE (Fragment). OS Zea mays (Maize). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophytida; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; OC Panicoideae; Andropogoneae; Zea. OX NCBI_TaxID=4577; RN [1] RP SEQUENCE. RC TISSUE=Coleoptile; RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C., RA Perronnet J.-C., Zivy M., de Vienne D.; RT "The maize two dimensional gel protein database: towards an integrated genome analysis program"; RT Theor. Appl. Genet. 93:987-1005(1996). CC -1 MISCELLANEOUS ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa. CC DR Maize2DPAGE: P80638; COLEOPTILE. DR MaizeB; 123954; - FT NON_TER 1 1 FT NON_TER 5 5 SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;	Query Match Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 EV 2 Db 4 EV 5	Qy 6 AE 7 Db 4 AE 5
RESULT 4			
FARP_MONEX ID FARP_MONEX STANDARD; PRT; 6 AA. AC P41966; DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1997 (Rel. 35, Last annotation update) DE FMRFamide-like neuropeptide GNFRFR amide. OS Moniezia expansa (Sheep tapeworm). OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda; OC Cyclopiliidea; Anoplocephalidae; Moniezia. OX NCBI_TaxID=28841;	Query Match Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 EV 2 Db 4 EV 5	Qy 6 AE 7 Db 4 AE 5
RESULT 5			
UN06_CLOPA ID UN06_CLOPA STANDARD; PRT; 6 AA. AC PB1351; DT 15-JUL-1998 (Rel. 36, Created) DT 15-JUL-1998 (Rel. 36, Last sequence update) DT 15-JUL-1998 (Rel. 36, Last annotation update) DE Unknown protein CP 6 from 2D-page (Fragment). OS Clostridium pasteurianum. OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; OC Clostridium OC NCBITaxID=1501; OX [1] RP SEQUENCE. RC STRAIN=W5; MEDLINE=98291870; PubMed=9629918; RA Flengsrød R., Skjeldal L.; RT two-dimensional gel electrophoresis separation and N-terminal sequencing analysis of proteins from Clostridium pasteurianum W5."; RL Electrophoresis 19:802-806(1998). CC -1 MISCELLANEOUS ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa. CC FT NON_TER 6 6 SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;	Query Match Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 EV 2 Db 4 EV 5	Qy 6 AE 7 Db 4 AE 5
RESULT 6			
AL14_CARMA ID AL14_CARMA STANDARD; PRT; 5 AA. AC PB1817; DT 30-MAY-2000 (Rel. 39, Created) DT 30-MAY-2000 (Rel. 39, Last sequence update) DT 30-MAY-2000 (Rel. 39, Last annotation update) DE Carcinustarin 14. OS Carcinus maenas (Common shore crab) (Green crab). OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Crustacea; OC Malacostraca; Eumalacostraca; Eucaridea; Decapoda; Pleocyemata; OC Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus. OX NCBITaxID=6759; RN [1] RP SEQUENCE. RC TISSUE=cerebral ganglion, and thoracic ganglion; RX MEDLINE=98121193; PubMed=9461295; RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.; RT Isolation and identification of multiple neuropeptides of the allatoxin superfamily in the shore crab <i>Carcinus maenas</i> ."; RL Eur. J. Biochem. 250:727-734(1997). CC -1 FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR. CC -1 SIMILARITY: BELONGS TO THE ALLATOCTATIN FAMILY. KW Neuropeptide; Amidation; Multigene family. FT MOD_RES 5 5 SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;	Query Match Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 EV 2 Db 4 EV 5	Qy 6 AE 7 Db 4 AE 5

Db	2 K 2	
RESULT 10		
ID	EI03_LITRU	STANDARD;
AC	P82090;	PRT;
DT	15-JUN-2002 (Rel. 41, Created)	5 AA.
DT	15-JUN-2002 (Rel. 41, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Electrin 3.	
OS	Litoria rubella (Desert tree frog)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelostomi; Amphibia; Batrachia; Anura; Neobatrachia; Butoidea; Hyliidae;	
OC	Pelodytadinae; Litoria.	
OX	NCBI_TaxID=104895;	
RN	"Litoria electrica. Comparison with the skin peptides from Litoria rubella.";	
RL	Aust. J. Chem. 52:639-645(1999).	
CC	-1- SUBCELLULAR LOCATION: SECRETED	
KW	Amphibian skin; Amidation.	
FT	MOD_RES 5	AMIDATION.
SQ	SEQUENCE 5 AA; 630 MW; 668761FC9A00000 CRC64;	
Query Match	10.0%; Score 1; DB 1; Length 5;	
Best Local Similarity	100.0%; Pred. No. 1.1e+05;	
Matches	1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	8 F 8	
Db	1 F 1	
RESULT 11		
ID	EI04_LITRU	STANDARD;
AC	P82100;	PRT;
DT	15-JUN-2002 (Rel. 41, Created)	5 AA.
DT	15-JUN-2002 (Rel. 41, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Electrin 4.	
OS	Litoria rubella (Desert tree frog)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelostomi; Amphibia; Batrachia; Anura; Neobatrachia; Butoidea; Hyliidae;	
OC	Pelodytadinae; Litoria.	
OX	NCBI_TaxID=104895;	
RN	"Peptides from the skin glands of the Australian buzzing tree frog Litoria rubella (Rel. 41)."	
RP	SEQUENCE.	
RC	TISSUE-Skin secretion;	
RA	Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;	
RT	Litoria electrica. Comparison with the skin peptides from Litoria rubella.	
RL	Aust. J. Chem. 52:639-645(1999).	
CC	-1- SUBCELLULAR LOCATION: SECRETED	
KW	Amphibian skin; Amidation.	
FT	MOD_RES 5	AMIDATION.
SQ	SEQUENCE 5 AA; 616 MW; 61F2D1A59A00000 CRC64;	
Query Match	10.0%; Score 1; DB 1; Length 5;	
Best Local Similarity	100.0%; Pred. No. 1.1e+05;	
Matches	1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	8 F 8	
Db	1 F 1	
RESULT 12		
ID	FARP_ARTTR	STANDARD;
AC	P41853;	PRT;
DT	01-NOV-1995 (Rel. 32, Last sequence update)	5 AA.
DT	01-NOV-1995 (Rel. 32, Last annotation update)	
DE	FMRamide-like neuropeptide RYRF-amide.	
OS	Artioposthia triangulata.	
OC	Eukaryota; Metazoa; Platynelminthes; Turbellaria; Seriata; Triciadida; Terricola; Geoplanae; Arthurdendyus.	
OX	NCBI_TaxID=132421;	
RN	[1]	
RP	SEQUENCE, AND SYNTHESIS.	
RX	MEDLINE-94211927; Pubmed=7909164;	
RA	Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;	
RT	"RYRFamide: a turbellarian FMRFamide-related peptide (FARP)." Regul. Pept. 50:37-43(1994).	
CC	-1 SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.	
KW	Neuropeptide; Amidation.	
FT	MOD_RES 5	AMIDATION.
SQ	SEQUENCE 5 AA; 754 MW; 69D404B44600000 CRC64;	
Query Match	10.0%; Score 1; DB 1; Length 5;	
Best Local Similarity	100.0%; Pred. No. 1.1e+05;	
Matches	1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RESULT 13		
ID	PAP2_PARMA	STANDARD;
AC	PB1864;	PRT;
DT	30-MAY-2000 (Rel. 39, Last sequence update)	5 AA.
DT	30-MAY-2000 (Rel. 39, Last annotation update)	
DE	Pardaxin II (PXXII) (Fragment).	
OS	Pardachirus marmoratus (Red sea moses sole).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostei; Neoteleostei; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes; Soleoidei; Soleidae; Pardachirus.	
OC	NCBI_TaxID=31087;	
RN	[1]	
RP	SEQUENCE.	
RC	TISSUE-Skin secretion;	
RX	MEDLINE-8705369; Pubmed=3782138;	
RA	Lazarovici P., Primor N., Loew L.M.;	
RT	"Purification and pore-forming activity of two hydrophobic polypeptides from the secretion of the Red sea moses sole (Pardachirus marmoratus)." J. Biol. Chem. 261:16704-16713(1986).	
RT	PROPERTIES. EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.	
CC	-1- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.	
CC	-1- SUBCELLULAR LOCATION: Secreted.	
CC	-1- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.	
KW	Toxin.	
FT	NON_TER 5	5
SQ	SEQUENCE 5 AA; 614 MW; 77699C9C8100000 CRC64;	
Query Match	10.0%; Score 1; DB 1; Length 5;	
Best Local Similarity	100.0%; Pred. No. 1.1e+05;	
Matches	1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	8 F 8	
Db	2 F 2	

RESULT 14

PRCT_PPERAM	STANDARD;	PRT;	5 AA.
ID P01373;			
AC			
DT 21-JUL-1986	(Rel. 01, Created)		
DT 21-JUL-1986	(Rel. 01, Last sequence update)		
DT 01-FEB-1995	(Rel. 31, Last annotation update)		
DE Proctolin.			
OS Periplaneta americana (American cockroach), Limulus polyphemus (Atlantic horseshoe crab), and Carcinus maenas (Common shore crab) (Green crab).			
OS Carcinus maenas (Common shore crab) (Green crab).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachii; Anura; Neobatrachia; Bufonoidea; Hyliidae; Pelodryadinae; Litoria.			
NCBI_TaxID=104895;			
RN [1]			
RP SEQUENCE.			
RC SPECIES=P.americana;			
RX MEDLINE=76074708; PubMed=576;			
RA Starratt A.N.; Brown B.E.; RT Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects.;			
RT Life Sci. 17:1253-1256(1975).			
RL [2]			
RN [3]			
RP BIOLOGICAL SOURCE.			
RC SPECIES=P.americana;			
RX MEDLINE=811225865; PubMed=6113690;			
RA O'Shea M.; Adams M.E.; RT Pentapeptide (proctolin) associated with an identified neuron.;			
RL Science 213:567-569(1981).			
RN [4]			
RP SEQUENCE.			
RC SPECIES=L.polyphemus;			
RX MEDLINE=90287800; PubMed=2356151;			
RA Groome J.R.; Tillinghast E.K.; Townley M.A.; Vetrov A.;			
RA Watson W.H. III; Hunt D.F.; Griffin P.R.; Alexander J.E.,			
RA Shabanowitz J.;			
RT Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus.;			
RL Peptides 11:205-211(1990).			
RN [5]			
RP SEQUENCE.			
RC SPECIES=C.maenas;			
RX MEDLINE=88232759; PubMed=2872661;			
RA Stangler J.; Dirksen H.; Keller R.;			
RT Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, <i>Carcinus maenas</i> .;			
RL Peptides 7:67-72(1986).			
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,			
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS,			
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN THE CRAB PERICARDIAL ORGANS.			
DR PIR: A01644; HOROHA.			
DR PIR: A60411; A60411.			
KW Neuropeptide.			
SQ SEQUENCE 5 AA: 649 MW: 71B7673B44600000 CRC64;			
Qy 9 R 9			
Db 1 R 1			

RESULT 15

RE11_LITTRU	STANDARD;	PRT;	5 AA.
ID RE11_LITTRU			
AC P82070;			
DT 15-JUN-2002 (Rel. 41, Created)			



protein - protein search, using sw model						
on:		April 21, 2003, 12:13:41 ; Search time 14 Seconds (without alignments)				
file: US-09-580-018-5						68.667 Million cell updates/sec
effect score: 10						EVKMDAEFRH 10
string table:	OLIGO	GapOp 60.0 , Gapext 60.0				
searched:	283224 seqs,	96134422 residues				
and size :	0					
total number of hits satisfying chosen parameters: 230						
minimum DB seq length: 5						
maximum DB seq length: 6						
t-processing: Listing first 45 summaries						
database :	PIR.73;*					
	1: pir1;*					
	2: pir2;*					
	3: pir3;*					
	4: pir4;*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.						
SUMMARIES						
8	Query ID	Match Length	DB ID	Score	Ult. No.	Description
1	2	20.0	5	2	A32516	cholecystokinin
	2	20.0	5	2	C23751	spinal cord peptide
	3	20.0	5	2	B41225	copper resistance
	4	20.0	5	2	B31835	20K protein - Rb
	5	20.0	5	2	FQ0009	angiotensin-converting
	6	20.0	5	2	B37988	acid proteinase
	7	20.0	5	2	A44692	fulmin - giant
	8	20.0	5	2	PT0596	T-cell receptor
	9	20.0	5	2	PT0538	T-cell receptor
	10	20.0	6	2	S02617	alcohol dehydrogenase
	11	20.0	6	2	S11024	hydroxensulfite
	12	20.0	6	2	A20186	fatty acid synthase
	13	20.0	6	2	A46474	Fc epsilon RIIB
	14	20.0	6	2	PT0616	T-cell receptor
	15	20.0	6	2	PT0687	T-cell receptor
	16	20.0	6	2	PT0650	T-cell receptor
	17	20.0	6	2	PT0550	T-cell receptor
	18	20.0	6	2	PT0587	T-cell receptor
	19	20.0	6	2	PT0588	T-cell receptor
	20	20.0	6	2	PT0693	neuropeptide GMP receptor
	21	20.0	6	2	A43129	procotolin - Amer
	22	10.0	5	1	HOROHA	glycoen phosphotriesterase
	23	10.0	5	2	A60521	peptidyl-dipeptidase
	24	10.0	5	2	JN0862	peptidyl-dipeptidase
	25	10.0	5	2	JN0850	mitosis inhibitor
	26	10.0	5	2	A26830	copper resistance
	27	10.0	5	2	CA1225	copper resistance
	28	10.0	5	2	A41205	ERF2 protein - X
	29	10.0	5	2	ST0154	ERF2 protein - X

```

primase - Citrobac
biorin B - Citrobac
pap fimbrial regul
trM protein - Esc
flagellar protein
alkanal monooxygen
ribosomal protein
ribosomal protein
ribosomal protein
dnazX-like protein
major protein anti
major protein anti
major protein anti
endo-1,4-beta-xyla
R-phycocerythrin al
R-phycocerythrin ga

ALIGNMENTS

RESULT 1
A32516
cholecytokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; W
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain
A;Reference number: A32516; PMID:87153871; PMID:3826354
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <HSI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5'modified site: amidated carboxyl end (Phe) # status experimental

Query Match          20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+0; Mismatches 0; Indels 0; Gaps 0
Matches 2; Conservative 0; Misaligned 0

QY      4 MD 5
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Db      3 MD 4

RESULT 2
C23751
spinal cord peptide SCP-6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C;Accession: C23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; PMID:85250425; PMID:4015098
A;Accession: C23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <HSI>
C;Superfamily: unassigned animal peptides

Query Match          20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+0; Mismatches 0; Indels 0; Gaps 0
Matches 2; Conservative 0; Misaligned 0

QY      5 DA 6
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Db      1 DA 2

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RESULT 3
B41225 copper resistance protein B - *Pseudomonas syringae* pv. tomato (fragment)
C;Species: *Pseudomonas syringae* pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: B41225
R;Cha, J. S.; Cooke, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in *Pseudomonas syringae* mediated by periplasmic and outer membrane protein.
A;Reference number: A41225; MUID:92020961; PMID:1924351
A;Accession: B41225
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CHa>

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 AE 7
Db 1 AE 2

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 AE 7
Db 1 AE 2

RESULT 4
B31836 20K protein - *Rickettsia rickettsii* (fragment)
C;Species: *Rickettsia rickettsii*
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C;Accession: B31836
R;Anderson, B.E.; Baumgard, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A;Title: Expression of the gene encoding the 17-kilodalton antigen from *Rickettsia rickettsii*
A;Reference number: A91885; MUID:89008059; PMID:3139629
A;Accession: B31836
A;Molecule type: DNA
A;Cross-references: GB:J03371; NTID:9152455; PIDN:AAD15030.1; PID:g4262874
A;Residues: 1-5 <AND>

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 MD 5
Db 1 MD 2

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 MD 5
Db 1 MD 2

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 VK 3
Db 4 VK 5

RESULT 5
PQ0009 angiotensin-converting enzyme inhibitor (PLP-2) - common fig
N:Alternative names: ficus latex Peptide 2
C;Species: *Ficus carica* (common fig)
C;Accession: PQ0009 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from *Ficus carica*.
A;Reference number: PQ0008
A;Accession: PQ0009
A;Molecule type: protein
A;Residues: 1-5 <MR>
A;Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 VK 3
Db 4 VK 5

RESULT 6
B37988 acid proteinase light chain - slime mold (*Physarum polycephalum*) (fragment)
C;Species: *Physarum polycephalum*
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C;Accession: B37988
R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, J. Biol. Chem. 265, 19898-19903, 1990
A;Title: Purification and characterization of a novel intracellular acid proteinase f
A;Reference number: A37988; MUID:91060608; PMID:2246266
A;Accession: B37988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <MR>
Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 AE 7
Db 1 AE 2

RESULT 7
A44692 fulicin - giant African snail (giant African snail)
C;Species: *Achatina fulica* (giant African snail)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C;Accession: A44692
R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; Biochim. Biophys. Res. Commun. 178, 486-493, 1991
A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from *Achatina fulica*, a giant African snail
A;Reference number: A44692; MUID:91315471; PMID:1859408
A;Accession: A44692
A;Molecule type: protein
A;Residues: 1-5 <OHT>
C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F;2/Modified site: D-asparagine (Asn) *status experimental
F;5/Modified site: amidated carboxyl end (Val) *status experimental
Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 EF 8
Db 3 EF 4

RESULT 8
PT0596 T-cell receptor beta chain V-D-J region (100-2AE) - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0596; PT0614
R;Feeoney, A.J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0596
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AE
A;Accession: PT0614
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DA 6
 Db 4 DA 5

RESULT 9
 PT0538
 T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Accession: PT0538; Pr0539; PT0603
 R;Feehey, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0538
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <PFE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
 A;Accession: PT0539
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <PFE3>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H
 A;Accession: Pr0603
 A;Status: translation not shown
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 A;Residues: 1-5 <PFE2>
 A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
 C:Keywords: T-cell receptor
 Query Match 20.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
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Qy 5 DA 6
 Db 4 DA 5

RESULT 10
 S02617
 alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
 C:Species: Equus caballus (domestic horse)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-1997
 C:Accession: S02617
 R;Fairwall, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joenvall
 FEBS Lett. 222, 99-103, 1987
 A;Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differences
 A;Reference number: S02617; MUID:88005160; PMID:3653405
 A;Accession: S02617
 A;Molecule type: protein
 A;Residues: 1-6 <PFAI>
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 20.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AE 7
 Db 2 AE 3

RESULT 11
 S11024
 hydrogensulfite reductase (EC 1.8.99.3) chain 1 - Desulfovibrio thermophilus (fragment)

N;Alternate names: bisulfite reductase; desulfofuscidin
 C;Species: Desulfovibrio thermophilus
 C;Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
 C:Accession: S11024
 R;Faigue, G.; Lino, A.R.; Czechowski, M.; Kang, I.; Dervartanian, D.V.; Moura, J.G.
 Biochim. Biophys. Acta 1040, 112-118, 1990
 A;Title: Purification and characterization of bisulfite reductase (desulfofuscidin)
 A;Reference number: S11024; MUID:90335276; PMID:2165817
 A;Accession: S11024
 A;Molecule type: protein
 A;Residues: 1-6 <FAU>
 C:Keywords: oxidoreductase

Query Match 20.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VK 3
 Db 3 VK 4

RESULT 12
 A20186
 fatty acid synthase (EC 2.3.1.85) - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 05-May-2000
 C:Accession: A20186
 R;McCarthy, A.D.; Aitken, A.; Hardie, G.; Santikarn, S.; Williams, D.H.
 FEBS Lett. 160, 296-300, 1983
 A;Title: Amino acid sequence around the active serine in the acyl transferase domain
 A;Reference number: A20186; MUID:6554204
 A;Accession: A20186
 A;Molecule type: protein
 A;Residues: 1-6 <MCC>
 C:Keywords: acyltransferase; coenzyme A

Query Match 20.0%; Score 2; DB 2; Length 6;
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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EV 2
 Db 4 EV 5

RESULT 13
 A46474
 FC epsilon RIb - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
 C:Accession: A46474
 R;Richards, M.L.; Katz, D.H.; Liu, F.T.
 J. Immunol. 147, 1067-1074, 1991
 A;Title: Complete genomic sequence of the murine low affinity Fc receptor for IgE. Dr
 A;Reference number: A46474; MUID:1861070
 A;Accession: A46474
 A;Status: Preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-6 <RIC>
 A;Experimental source: BALB C, splenic B cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:45428)

Query Match 20.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MD 5
 Db 1 MD 2

RESULT 14

PT0616
T-cell receptor beta chain V-D-J region (120-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R;Peeney, A. J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Accession: PT0616
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <PFB>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

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Qy	5 DA 6			
Db	4 DA 5			

RESULT 15

PT0687
T-cell receptor beta chain V-D-J region (120-2CM) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997
C;Accession: PT0687; PT0541
R;Peeney, A. J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Accession number: PT0609; PMID:91277601; PTID:1711558
A;Accession: PT0609
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <PFB>
A;Experimental source: newborn thymus, strain BALB/c, clone 140-1A
A;Accession: PT0687
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <PE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1A
A;Accession: PT0541
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <PE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c (clone A3/IIC7)
C;Keywords: T-cell receptor

Query Match	20.0%	Score 2;	DB 2;	Length 6;
Best Local Similarity	100.0%	Pred. No.	2.8e+05;	
Matches	2;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	5 DA 6			
Db	4 DA 5			

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 Copyright (c) 1993 - 2003 Compugen Ltd.
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 Perfect score: 10
 Sequence: EVKMDAEFRH 10
 Scoring table: OLIGO
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  Pred. No. is the number of results predicted by chance to have a  

  score greater than or equal to the score of the result being printed,  

  and is derived by analysis of the total score distribution.
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SUMMARIES

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3	5	50.0	5	10	US-09-794-743-72	Sequence 72, Appl
4	5	50.0	5	10	US-09-794-748-72	Sequence 72, Appl
5	5	50.0	5	10	US-09-794-925-72	Sequence 72, Appl
6	5	50.0	5	10	US-09-681-442-72	Sequence 72, Appl
7	4	40.0	6	10	US-09-808-037-7	Sequence 7, Appl
8	3	30.0	5	9	US-10-179-046-15	Sequence 15, Appl
9	3	30.0	5	10	US-09-071-938-209	Sequence 209, Appl
10	3	30.0	6	9	US-09-727-963A-21	Sequence 21, Appl
11	3	30.0	6	9	US-09-727-963A-87	Sequence 87, Appl
12	3	30.0	6	9	US-10-059-749-72	Sequence 72, Appl
13	3	30.0	6	9	US-10-247-488-8	Sequence 8, Appl
14	3	30.0	6	9	US-10-091-135-89	Sequence 89, Appl
15	3	30.0	6	10	US-09-065-086-230	Sequence 230, Appl
16	3	30.0	6	10	US-09-952-768-57	Sequence 57, Appl
17	3	30.0	6	10	US-09-954-997-10	Sequence 110, Appl
18	3	30.0	5	8	US-09-982-172-44	Sequence 20, Appl
19	2	20.0	5	8	US-08-859-699-20	Sequence 20, Appl

ALIGNMENTS

```
RESULT 1  

US-09-794-927-72  

; Sequence 72, Application US/09734927  

; Patent No. US201001634A1  

; GENERAL INFORMATION:  

; APPLICANT: Gurney, Mark E.  

; APPLICANT: Bienczkowski, Michael J.  

; APPLICANT: Heinrikson, Robert L.  

; APPLICANT: Farodi, Luis A.  

; APPLICANT: Wan, Riqiang  

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND  

; TITLE OF INVENTION: USES  

; TITLE OF INVENTION: THEREFOR  

; FILE REFERENCE: 28341/6280FC  

; CURRENT APPLICATION NUMBER: US-09/794,927  

; CURRENT FILING DATE: 2001-02-27  

; PRIOR APPLICATION NUMBER: 09/416,901  

; PRIOR FILING DATE: 1998-10-13  

; PRIOR APPLICATION NUMBER: 60/155,493  

; PRIOR FILING DATE: 1999-09-23  

; PRIOR APPLICATION NUMBER: 09/404,133  

; PRIOR FILING DATE: 1999-09-23  

; PRIOR APPLICATION NUMBER: PCT/US99/20881  

; PRIOR FILING DATE: 1999-09-23  

; PRIOR APPLICATION NUMBER: 60/101,594  

; NUMBER OF SEQ ID NOS: 73  

; SOFTWARE: Patentin Ver. 2.0  

; SEQ ID NO: 72  

; LENGTH: 5  

; TYPE: PRT  

; ORGANISM: Artificial sequence  

; FEATURE:  

; OTHER INFORMATION: Description of Artificial Sequence: synthetic  

US-09-794-927-72
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QY 5 DAFFR
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Db      1 DAEFR 5

RESULT 2
; Sequence 72, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
;   APPLICANT: Gurney, Mark E.
;   APPLICANT: Bienkowski, Michael J.
;   APPLICANT: Heinrikson, Robert L.
;   APPLICANT: Parodi, Luis A.
;   APPLICANT: Yan, Riqiang
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;   TITLE OF INVENTION: USES
;   TITLE OF INVENTION: THEREFOR
;   FILE REFERENCE: 28341/6280DE
;   CURRENT APPLICATION NUMBER: US/09/795, 847
;   CURRENT FILING DATE: 2001-02-28
;   PRIOR APPLICATION NUMBER: 09/416,901
;   PRIOR FILING DATE: 1999-10-13
;   PRIOR APPLICATION NUMBER: 60/155,493
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 09/404,133
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: PCT/US99/20881
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 60/101,594
;   PRIOR FILING DATE: 1998-09-24
;   NUMBER OF SEQ ID NOS: 73
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 72
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-847-72

Query Match          50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 DAEFR 9
Db      1 DAEFR 5

RESULT 4
; Sequence 72, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
;   APPLICANT: Gurney, Mark E.
;   APPLICANT: Bienkowski, Michael J.
;   APPLICANT: Heinrikson, Robert L.
;   APPLICANT: Parodi, Luis A.
;   APPLICANT: Yan, Riqiang
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;   TITLE OF INVENTION: USES
;   TITLE OF INVENTION: THEREFOR
;   FILE REFERENCE: 28341/6280JL
;   CURRENT APPLICATION NUMBER: US/09/794,748
;   CURRENT FILING DATE: 2001-02-27
;   PRIOR APPLICATION NUMBER: 09/416,901
;   PRIOR FILING DATE: 1999-10-13
;   PRIOR APPLICATION NUMBER: 60/155,493
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 09/404,133
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: PCT/US99/20881
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 60/101,594
;   PRIOR FILING DATE: 1998-09-24
;   NUMBER OF SEQ ID NOS: 73
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 72
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-72

Query Match          50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 DAEFR 9
Db      1 DAEFR 5

RESULT 3
; Sequence 72, Application US/09794743
; Patent No. US2001021391A1
; GENERAL INFORMATION:
;   APPLICANT: Gurney, Mark E.
;   APPLICANT: Bienkowski, Michael J.
;   APPLICANT: Heinrikson, Robert L.
;   APPLICANT: Parodi, Luis A.
;   APPLICANT: Yan, Riqiang
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;   TITLE OF INVENTION: USES
;   TITLE OF INVENTION: THEREFOR
;   FILE REFERENCE: 28341/6280C
;   CURRENT APPLICATION NUMBER: US/09/794,743
;   CURRENT FILING DATE: 2001-02-27
;   PRIOR APPLICATION NUMBER: 09/416,901
;   PRIOR FILING DATE: 1999-10-13
;   PRIOR APPLICATION NUMBER: 60/155,493
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 09/404,133
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: PCT/US99/20881
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 60/101,594
;   PRIOR FILING DATE: 1998-09-24
;   NUMBER OF SEQ ID NOS: 73
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 72
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-743-72

Query Match          50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 DAEFR 9
Db      1 DAEFR 5

RESULT 5
; Sequence 72, Application US/09794925
; Patent No. US2002006481A1
; GENERAL INFORMATION:
;   APPLICANT: Gurney, Mark E.
;   APPLICANT: Bienkowski, Michael J.
;   APPLICANT: Heinrikson, Robert L.
;   APPLICANT: Parodi, Luis A.
;   APPLICANT: Yan, Riqiang
;   TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;   TITLE OF INVENTION: USES
;   TITLE OF INVENTION: THEREFOR
;   FILE REFERENCE: 28341/6280C
;   CURRENT APPLICATION NUMBER: US/09/794,925
;   CURRENT FILING DATE: 2001-02-27
;   PRIOR APPLICATION NUMBER: 09/416,901
;   PRIOR FILING DATE: 1999-10-13
;   PRIOR APPLICATION NUMBER: 60/155,493
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 09/404,133
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: PCT/US99/20881
;   PRIOR FILING DATE: 1999-09-23
;   PRIOR APPLICATION NUMBER: 60/101,594
;   PRIOR FILING DATE: 1998-09-24
;   NUMBER OF SEQ ID NOS: 73
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 72
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-72

Query Match          50.0%; Score 5; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
 ; FILE REFERENCE: 28341/6280H
 ; CURRENT APPLICATION NUMBER: US/09/794,925
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 72
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; US-09-794-925-72

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Qy	5	DAEFR 9						
	11111							
Db	1	DAEFR 5						

RESULT 6
 US-09-681-442-72
 ; Sequence 72, Application US/09681442
 ; Patent No. US20020081634A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Blenkowski, Michael J.
 ; APPLICANT: Heinriksson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
 ; FILE REFERENCE: 28341/6280FG
 ; CURRENT APPLICATION NUMBER: US/09/681,442
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 72
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; US-09-681-442-72

Query	Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
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	Matches	Best Local Similarity	100.0%	Pred. No.	2.6e+05;			
	5	Conservative	0;	Mismatches	0;	0	0	0;
Qy	5	DAEFR 9						
	11111							
Db	1	DAEFR 5						

RESULT 7
 US-09-808-037-7
 ; Sequence 7, Application US/09808037
 ; Patent No. US20020052311A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SOLOMON, Beka
 ; APPLICANT: HANAN, Billat
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSTICS OF NEUROLOGICAL DISEASES AND DISORDERS
 ; FILE REFERENCE: SOLOMON-2D
 ; CURRENT APPLICATION NUMBER: US/09/808,037
 ; CURRENT FILING DATE: 2001-03-15
 ; PRIOR APPLICATION NUMBER: 09/629,971
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: US/09/473,653
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: US 60/152,417
 ; PRIOR FILING DATE: 1999-09-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 ; US-09-808-037-7

Query	Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
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	Matches	Best Local Similarity	100.0%	Pred. No.	2.6e+05;			
	5	Conservative	0;	Mismatches	0;	0	0	0;
Qy	5	EFRH 10						
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Db	3	EFRH 6						

RESULT 8
 US-10-179-046-15
 ; Sequence 15, Application US/10179046
 ; Publication No. US2003013154A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Crawford, Kenneth
 ; APPLICANT: Zaror, Isabel
 ; APPLICANT: Innis, Michael
 ; TITLE OF INVENTION: Pichila Secretary Leader for Protein
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94608
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/179,046
 ; FILING DATE: 25-Jun-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/029,267

Query	Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps
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	Matches	Best Local Similarity	100.0%	Pred. No.	2.6e+05;			
	5	Conservative	0;	Mismatches	0;	0	0	0;
Qy	5	DAEFR 5						
	11111							
Db	1	DAEFR 5						

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 1165,100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2704
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-179-046-15

Query Match 30.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 3 KMD 5
Db 1 KMD 3

RESULT 10
US-09-727-963A-21
; Sequence 21, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; ATTORNEY/AGENT INFORMATION:
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIORITY FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence : peptide

Qy 7 EFR 9
Db 3 EFR 5

RESULT 9
US-09-071-838-209

Query Match 30.0%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 8 FRH 10
Db 4 FRH 6

RESULT 11
US-09-727-963A-87
; Sequence 87, Application US/09727963A
; Patent No. US20020155106A1
; GENERAL INFORMATION:
; APPLICANT: V.I. Technologies, Inc.
; ATTORNEY/AGENT INFORMATION:
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE
; FILE REFERENCE: 18242-505
; CURRENT APPLICATION NUMBER: US/09/727,963A
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557
; PRIORITY FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 87
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence : peptide

Qy 1 EVK 3

Db 3 111 ; SEQ ID NO: 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Humanus
; US-10-247-488-8

RESULT 12
; Sequence 72, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Almehri, Emad S.
; Fernando-Almehri, Teresa
; Litzwak, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
; US-10-059-749-72

Query Match 30.0%; Score 3; DB 9; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.6e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; General Information:
; Qy 7 EFR 9
; Db 1 111 EFR 3

RESULT 13
; Sequence 8, Application US/10247488
; Publication No. US2003002244A1
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336-RAMOT
; CURRENT APPLICATION NUMBER: US/10/247,488
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/526,738
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1

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; Best Local Similarity 100.0%; Pred. No. 2.6e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; General Information:
; Qy 8 FRH 10
; Db 1 111 FRH 3

RESULT 14
; US-10-091-135-89
; Sequence 89, Application US/10091135
; Publication No. US2003039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; APPLICANT: Title of Invention: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
; FILE REFERENCE: 2213/311587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIORITY APPLICATION NUMBER: US 60/272,818
; PRIORITY FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 89
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
; US-10-091-135-89

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; Best Local Similarity 100.0%; Pred. No. 2.6e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; General Information:
; Qy 6 AEF 8
; Db 4 111 AEF 6

RESULT 15
; US-09-765-086-230
; Sequence 230, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Vadim, Arap
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerdy, H. Michael
; APPLICANT: Title of Invention: Chimeric Prostate-Homing Peptides With Pro-Apoptotic Activity
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIORITY APPLICATION NUMBER: US 09/4489,582
; PRIORITY FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 230
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide

us-09-765-086-230

Query Match 30.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVK 3
 |
 |
Db 2 EVK 4

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Job time : 15 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:13:01 ; Search time 14 Seconds
(without alignments)
21.016 Million cell updates/sec

Title: US-09-580-018-5
Perfect score: 10
Sequence: 1 EVKMDAEFRH 10

Scoring table: Oligo Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query ID	Description
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2	50.0	5 2 US-09-422-313-7	Sequence 7, Appli
3	50.0	5 4 US-09-659-984A-13	Sequence 13, Appli
4	50.0	5 4 US-09-660-531-13	Sequence 1, Appli
5	50.0	5 4 US-09-054-334-1	Patent No. 5187153
6	50.0	5 6 5187153-6	Patent No. 5220013
7	50.0	5 6 5223013-6	Patent No. 5223082
8	50.0	5 6 52230182-6	Sequence 3, Appli
9	40.0	6 1 US-07-965-971-3	Sequence 3, Appli
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12	40.0	6 1 US-08-440-423-3	Sequence 3, Appli
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14	40.0	6 3 US-08-846-844-3	Sequence 3, Appli
15	30.0	5 1 US-08-297-330-11	Sequence 11, Appli
16	30.0	5 2 US-08-719-758-16	Sequence 16, Appli
17	30.0	5 3 US-08-637-759B-303	Sequence 303, Appli
18	30.0	5 3 US-08-871-355A-303	Sequence 303, Appli
19	30.0	5 3 US-09-029-267-15	Sequence 15, Appli
20	30.0	5 4 US-09-119-827-16	Sequence 16, Appli
21	30.0	5 4 US-09-177-249-209	Sequence 209, Appli
22	30.0	5 4 US-09-001-984C-24	Sequence 24, Appli
23	30.0	5 4 US-09-117-121-9	Sequence 9, Appli
24	30.0	5 4 US-09-201-245-303	Sequence 303, Appli
25	30.0	5 4 US-09-187-859-116	Sequence 116, Appli
26	30.0	5 4 US-09-187-859-117	Sequence 117, Appli
27	30.0	5 4 US-09-187-859-119	Sequence 119, Appli

ALIGNMENTS

RESULT 1
US-09-480-498-1
; Sequence 1, Application US/08480498
; Patent No. 574446
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M. S.
; SINHA, Sulavanto
; REIM, Pamela S.
; KEIM, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,498
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-480-498-1

Query Match 50.0%; Score 5; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6
Db 1 VKMDA 5

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RESULT 2
US-08-422-333-7
; Sequence 7, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94031

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; TELEFAX: (415) 968-2438
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-422-333-7

Query Match      50.0%: Score 5; DB 2; Length 5;
Best Local Similarity 100.0%: Pred. No. 2e+05; Mismatches 0; Indels 0; Caps 0;
Matches 5; Conservative 0; Inhibition 21;

QY 4 MDAEF 8
DB 1 MDAEF 5

RESULT 3
US-08-659-984A-13
; Sequence 13, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta - Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-13

Query Match 50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6
Db 1 VKMDA 5

RESULT 5
US-09-034-334-1
Sequence 1, Application US/09054334
Patent No. 632963

GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Jacobson-Croak, Kirsten L.
APPLICANT: Sinha, Sukanto

TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09/054,334
FILING DATE: 02-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 015270-002820US
TELECOMMUNICATION INFORMATION:
PHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-054-334-1

Query Match 50.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6
Db 1 VKMDA 5

RESULT 5
US-07/502,273
NUMBER OF SEQUENCES: 33
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/502,273
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 361,912
FILING DATE: 29-MAR-1990
APPLICATION NUMBER: 361,912
FILING DATE: 06-JUN-1989
APPLICATION NUMBER: 359,911
FILING DATE: 12-MAY-1989
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 6:
5187153 LENGTH: 5

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAAFP 8
Db 1 MDAAFP 5

RESULT 7
5220013-6
Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO: 6:
5220013-6

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAAFP 8
Db 1 MDAAFP 5

RESULT 8
5223482-6
; Patent No. 5223482
; APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL,
; BARBARA
; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
; NUMBER OF SEQUENCES: 34

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 359,911
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:6;
; LENGTH: 5
; 5223482-6

Query Match 50.0%; Score 5; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDAEF 8
Db 1 MDAEF 5

RESULT 9
US-07-965-971-3
; Sequence 3, Application US/07965971
; Patent No. 5414870
; GENERAL INFORMATION:
; APPLICANT: Seubert, Peter A.
; APPLICANT: Schenk, Dale B.
; APPLICANT: Fritz, Lawrence C.
; TITLE OF INVENTION: Methods and Compositions for Monitoring
; Cellular Processing of Beta-Amyloid Precursor Protein
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,697
FILING DATE: 27-OCT-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/965,971
FILING DATE: 26-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/868,949
FILING DATE: 15-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
TELEPHONE: 415-326-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
TELEFAX: 415-326-2400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-143-697-3

Query Match 40.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKM 4
Db 3 EVKM 6

RESULT 11
US-08-440-261-3
; Sequence 3, Application US/08440261
; Patent No. 5605811
; GENERAL INFORMATION:
; APPLICANT: Seubert, Peter A.

US-07-965-971-3

APPLICANT: Schenk, Dale B.
 APPLICANT: Fritz, Lawrence C.
 TITLE OF INVENTION: Methods and Compositions for Monitoring
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/440,261
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/965,971
 FILING DATE: 26-OCT-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Heslin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15270-4-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2422
 TELEXFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-440-261-3

Query Match 40.0%; Score 4; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKM 4
 Db 1111
 3 EVKM 6

RESULT 12
 US-08-440-423-3
 Sequence 3, Application US/08440423
 Patent No. 5721130
 GENERAL INFORMATION:
 APPLICANT: Seubert, Peter A.
 APPLICANT: Schenk, Dale B.
 APPLICANT: Fritz, Lawrence C.
 TITLE OF INVENTION: Methods and Compositions for Monitoring
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 26-FEB-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jarrell Ph.D., Brenda H.
 REGISTRATION NUMBER: 39,223
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 248 5000
 TELEXFAX: 617 248 4000
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 US-08-025-321C-2

Query Match 40.0%; Score 4; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKM 4 ; Sequence 11, Application US/08297330
 Db 3 EVKM 6 ; Patent No. 5593108

RESULT 14 ; GENERAL INFORMATION:
 US-08-846-444-3 ; APPLICANT: Seibert, Peter A.
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Fritz, Lawrence C.
 ; TITLE OF INVENTION: Methods and Compositions for Monitoring
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/846,444
 ; FILING DATE: No. 6018024 yet assigned
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/868,949
 ; FILING DATE: 15-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/965,971
 ; FILING DATE: 26-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US93/01817
 ; FILING DATE: 03-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/440,423
 ; FILING DATE: 12-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storlila, John R.
 ; REGISTRATION NUMBER: 32,-944
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-846-444-3 ; Query Match 40.0%; Score 4; DB 3; Length 6;
 ; Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKM 4 ; Sequence 11, Application US/08297330
 Db 3 EVKM 6 ; Patent No. 5593108

RESULT 15

US-08-297-330-11 ; General Information:
 ; Sequence 11, Application US/08297330
 ; Patent No. 5593108
 ; General Information:
 ; APPLICANT: Wei, Chi-Ming
 ; APPLICANT: Burnett, John C.
 ; Title of Invention: Vasonatrin Peptide and Analogs
 ; Title of Invention: Thereof
 ; Number of Sequences: 17
 ; Correspondence Address:
 ; Addressee: Merchant & Gould
 ; Street: 3100 No. 5583108west Center
 ; City: Minneapolis
 ; State: MN USA
 ; Zip: 55402-4131
 ; Computer Readable Form:
 ; Medium Type: Floppy disk
 ; Computer: IBM PC compatible
 ; Operating System: PC-DOS/MS-DOS
 ; Software: PatentIn Release #1.0, Version #1.25
 ; Current Application Data:
 ; Application Number: US/08/297,330
 ; Filing Date:
 ; Classification: 514
 ; Prior Application Data:
 ; Application Number: US 08/025,935
 ; Filing Date: 03-MAR-1993
 ; Attorney/Agent Information:
 ; Name: Woessner, Warren D.
 ; Registration Number: 30,440
 ; Reference/DoCet Number: 1016.99-US01
 ; Telecommunication Information:
 ; Telephone: 612-332-5300
 ; Telex/Fax: 612-332-9081
 ; Information for Seq Id No: 11:
 ; Sequence Characteristics:
 ; Length: 5 amino acids
 ; Type: amino acid
 ; Strandedness: single
 ; Topology: linear
 ; Molecule Type: peptide

US-08-297-330-11 ; Query Match 30.0%; Score 3; DB 1; Length 5;
 ; Best Local Similarity 100.0%; Pred. No. 2e+05; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 KMD 3 ; Job time : 14 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:10:31 ; Search time 34 Seconds

(without alignments)
39.191 Million cell updates/secTitle: US-09-580-018-5
Perfect score: 10
Sequence: EVKMDAEFFH 10

Scoring table: Oligo Gapext 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

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Total number of hits satisfying chosen parameters: 30890

Minimum DB seq length: 5

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	6	60.0	6	19	AAV70868	Beta amyloid peptide
2	6	60.0	6	23	AAU78525	Beta amyloid precursor protein
3	5	50.0	5	14	AAV37864	Beta amyloid peptide
4	5	50.0	5	18	AAW08216	Wild type APP beta
5	5	50.0	5	19	AAW061150	Wild-type APP cleavage
6	5	50.0	5	20	AAV373750	Wild type beta-amyloid precursor protein promoter
7	5	50.0	5	20	AAV08608	Beta APP alpha secretase
8	5	50.0	5	21	AAV69702	Human APP Sw mutant
9	5	50.0	5	22	AAE10667	Human Asp-2 beta-synuclein
10	5	50.0	5	22	AAE06907	

Synthetic.

Homo sapiens.

PN WO9844955-A1.

XX XX

Peptide product of Human beta-amyloid Wild type APP sequ	5	22	AAU06636
Beta-secretase rel	5	22	AB47260
Amyloid protein pr	5	23	AB06534
Beta-amyloid pepit	5	23	AB00579
Human APP A-beta 1	6	19	AAW70864
Human amyloid beta	6	22	AB46199
Peptide representati	6	22	AB49095
Human amyloid beta	6	22	AAW8241
Epitope #1 used in C-terminal arm of Pentapeptide paral	6	22	AB47109
Mimotope peptide #	5	10	APR91846
Peptide signal seq	5	15	ARR42248
TK SH2 association	5	15	ARR52938
Natriuretic peptide	5	15	ARR71638
Fulicin-like neuro	5	16	ARR93907
Fulicin-like neuro	5	16	ARR51592
Pentameric mimot	5	16	ARR59380
Cyclic pentapeptid	5	16	ARR69360
Peptide 86 from 88	5	17	AAW09844
P. americanus skin	5	17	AAW98706
IDA-peptide capabl	5	18	AAW22867
Neuropeptide. Ach	5	18	AAW12322
Peptide produced b	5	19	AAW70127
Human delta-sarcog	5	19	AAW67458
Linker used to fin	5	20	AAW62779
Peptide derived fr	5	21	AAV44411
Cadherin-5 cell ad	4	21	AAV60878
Cadherin-5 cell ad	4	21	AAV60879
Cadherin-5 cell ad	4	21	AAV60881
Cadherin-5 cell ad	4	21	AAV60890

ALIGNMENTS

RESULT 1	AAW70868
ID	AAW70868 standard; peptide: 6 AA.
XX	
AC	AAW70868;
XX	04-FEB-1999 (first entry)
DT	
XX	Beta-amyloid peptide to create a monoclonal antibody.
DE	
XX	Beta-amyloid precursor protein; beta-APP; beta-amyloid peptide; antibody; amyloid deposit; Alzheimer's disease.
OS	
XX	Synthetic.
XX	
PN	WO9844955-A1.
XX	
PD	15-OCT-1998.
XX	
PF	09-APR-1998;
PR	09-APR-1997;
XX	98WO-US06900.
PA	(MCINN/ MCINNIS P A.
PA	(MIND/ MINDSET LTD.
XX	
PI	Chain DG;
DR	WPI: 1998-594476/50.
XX	
XX	Preventing or inhibiting progression of Alzheimer's Disease - comprises use of recombinant DNA encoding an antibody specific for

PT the N- or C-terminus of an amyloid-beta peptide
 XX Example 1; Page 47; 58pp; English.

CC The present sequence represents a peptide derived from beta-amyloid
 CC precursor protein (beta-APP, see AAW70363). The peptide is a
 CC beta-amyloid peptide and is used to produce a monoclonal antibody. The
 CC progression of Alzheimer's disease. The method comprises administering a
 CC recombinant DNA molecule containing a gene
 CC encoding a recombinant antibody end-specific for the N-terminus or the
 CC C-terminus of an amyloid-beta peptide, operably linked to a promoter
 CC which is expressed in the central nervous system. The recombinant
 CC antibody molecules prevent the accumulation of beta-amyloid peptides in
 CC the extracellular space, interstitial fluid and cerebrospinal fluid and
 CC the aggregation of such peptides into amyloid deposits in the brain.
 CC They also inhibit the progression of Alzheimer's disease by inhibiting
 CC the interaction of beta-amyloid peptides mediating Alzheimer's disease induced
 CC induced neurotoxicity and inhibiting the Alzheimer's disease induced
 CC complement activation and cytokine release involved in the inflammatory
 CC process.

XX Sequence 6 AA;

Query Match Score 6;	DB 19;	Length 6;
Best Local Similarity 100 %;	Pred. No. 7.8e+05;	
Matches 6;	Conservative 0;	Mismatches 0;
AC AAAU78525;	Indels 0;	Gaps 0;

QY 5 DAEFRH 10
 |||||
 Db 1 DAEFRH 6

RESULT 2
 ID AAU78525 standard; Peptide: 6 AA.
 XX
 AC
 XX DT 18-JUN-2002 (first entry)
 DE Beta amyloid precursor protein beta secretase cleavage site.
 XX
 KW Alzheimer's disease; beta amyloid precursor protein; beta secretase;
 KW BACE; beta-site APP cleaving enzyme; nootropic; neuroprotective;
 KW beta-site amyloid precursor protein (APP)-cleaving enzyme; APP;
 KW BACE secretase/sheddase; neurodegenerative disorder.
 XX
 OS Unidentified.
 XX
 FH Location/Qualifiers 4..5
 FT Cleavage-site /note= "Beta secretase cleavage site"
 XX
 PN WO200210354-A2.
 XX
 PD 07-FEB-2002.
 XX
 FF 01-AUG-2001; 2001WO-CA01118.
 XX
 PR 01-AUG-2000; 2000CA-2313828.
 XX
 PA (REGL-) INST RECH CLINIQUES MONTREAL.
 XX
 PI Seidah NG, Chretien M, Cromlish JA;
 XX
 DR WPI; 2002-2B0632/32.
 XX
 PT Modulating activity of beta-site amyloid precursor protein protease-cleaving
 PT enzyme/sheddase for treatment of neurodegenerative disorder
 PT characterised by generation of Abeta peptide, by preventing cleavage of
 PT enzyme -

PS Disclosure; Page 2; 64pp; English.

CC This invention relates to a novel method for modulating activity of
 CC beta-site amyloid precursor protein (APP)-cleaving enzyme (BACE)
 CC secretase/sheddase. Cleavage of BACE by this enzyme results in the
 CC generation of a soluble BACE which enhances the production of the
 CC amyloidogenic peptide Abeta which has been shown to be involved in the
 CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
 CC achieved by administration of an antisense nucleotide molecule capable
 CC of hybridising with BACE mRNA, by using a ribozyme that targets and
 CC degrades BACE secrete mRNA, with a peptide that can interfere with
 CC binding of the enzyme with BACE or using an antibody or antagonist that
 CC can function as an inhibitor of BACE secretase activation. The methods
 CC of the invention modulate the activity of BACE secretase/sheddase by
 CC preventing cleavage of BACE, which is useful for the treatment of a
 CC neurodegenerative disorder characterised by the generation of Abeta
 CC protein, especially Alzheimer's disease. The invention also comprises a
 CC method for identification of an agent that can alter the ability of BACE
 CC secretase to associate with and process a known substrate, this method
 CC can be used for high throughput screening of candidate molecules. The
 CC invention also comprises a method for determining whether an individual
 CC is at risk of developing a neurodegenerative disorder characterised
 CC by the generation of Abeta protein by measuring the levels of BACE
 CC terminal cleavage products in a sample or tissue where an increase
 CC in cleavage products indicates a person at risk. The present sequence
 CC sequence represents the beta amyloid precursor protein (APP) beta
 CC secretase cleavage site important for beta APP processing.

SQ Sequence 6 AA;

Query Match Score 60.0%;	DB 23;	Length 6;
Best Local Similarity 100.0%;	Pred. No. 7.8e+05;	
Matches 6;	Conservative 0;	Mismatches 0;
AC	Indels 0;	Gaps 0;

QY 1 EVKMDA 6
 |||||
 Db 1 EVKMDA 6

RESULT 3
 AAR37864
 ID AAR37864 standard; Protein; 5 AA.
 XX
 AC AAR37864;
 XX DT 27-OCT-1993 (first entry)
 DE Beta amyloid protein N-terminal peptide deduced from clone SM2W4.
 XX
 KW Alzheimer's Disease; Amyloid Plaque Core Protein; APCP;
 KW neuritic plaque.
 XX
 OS Homo sapiens.
 XX
 PN US5220013-A.
 XX
 PD 15-JUN-1993.

XX
 PF 17-NOV-1986; 86US-0932193.
 XX
 PR 17-NOV-1986; 86US-0932193.
 PR 31-DEC-1986; 86US-0948376.
 PR 30-JAN-1987; 87US-0008810.
 PR 18-AUG-1987; 87US-0087002.
 PR 30-NOV-1989; 89US-044118.
 XX
 PA (SCIO) SCIOS NOVA INC.
 XX
 PI Cordell B, Ponte PA;
 XX
 DR WPI; 1993-205383/25.
 DR N-PSDB; AAQ42663.

XX PN WO9964587-A1.
 XX
 PD 16-DEC-1999.
 XX PR 04-JUN-1999; 99WO-FR01326.
 XX PR 05-JUN-1998; 98FR-0007068.
 PR 31-MAR-1999; 99US-012599.
 XX PA (RHON) RHONE-POULENC RORER SA.
 PA (UYPKA-) UNIV CURIE PARIS VI P & M.
 PI Rholam M, Munoz-Gimenez N, Moutauakil M, Cohen P, Bertrand P;
 DR 2000-097537/08.
 XX PT Polypeptide with beta-secretase activity, specific for wild-type
 PT amyloid precursor protein, useful in treating Alzheimer's disease
 XX PS Example 3; Page 24; 44pp; French.
 XX Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
 CC novel polypeptide with beta-secretase activity that can cleave
 CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
 CC cleavage of the protein occurs between amino acids Met506-Asp597 and
 CC Val536-Tle637 (positions 4-5 and 44-45 of AY69701). The novel
 CC polypeptide is used to identify agents that interact specifically with
 CC it. These agents regulate metabolism of APP, particularly they slow down
 CC or reduce production of beta-amyloid, so can be used to treat
 CC neurodegenerative diseases, particularly Alzheimer's disease.
 XX SQ Sequence 5 AA:
 Query Match 50.0%; Score 5; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 DAEFR 9
 Db 1 DAEFR 5
 RESULT 9
 AAE10667
 ID AAE10667 standard; peptide; 5 AA.
 XX AC AAE10667;
 XX DT 10-DEC-2001 (first entry)
 XX DE Human APP-Sw mutant beta-secretase substrate peptide #1.
 KW Human; aspartyl protease 1; Asp1; amyloid precursor protein;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
 KW APP-Sw beta-secretase peptide; mutant; mutenin.
 OS Homo sapiens.
 XX PN GB2357767-A.
 PD 04-JUL-2001.
 XX PF 22-SEP-2000; 2000GB-0023315.
 XX PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0410413.
 PR 13-OCT-1999; 99WO-US2081.
 PR 06-DEC-1999; 99US-0416801.
 PR 06 DEC-1999; 99US-0169332.
 XX PA (PHAA) PHARMACIA & UPJOHN CO.

XX BIENKOWSKI MJ, GURNEY M;
 PI XX
 DR XX
 PT XX
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 PS Example 12; Page 84; 187pp; English.
 XX The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
 CC Asp1 proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Asp1 alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Asp1 alpha-secretase activity, where modulators that increase
 CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
 CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
 CC precursor protein Swedish (APP-Sw) mutant beta-secretase specific
 CC substrate peptide. This peptide is obtained by Swedish KM-NL mutation
 CC of human APP protein. This peptide is used for assaying the beta-
 CC secretase activity of human Aspartyl protease 2a (Asp2a) protein.
 CC The peptide is also used for determining the relationship between
 CC Asp1 and APP protein.
 XX SQ Sequence 5 AA;
 Query Match 50.0%; Score 5; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 DAEFR 9
 Db 1 DAEFR 5
 RESULT 10
 AAE06907
 ID AAE06907 standard; peptide; 5 AA.
 XX AC AAE06907;
 XX DT 23-OCT-2001 (first entry)
 XX DE Human Asp-2 beta-secretase activity assaying substrate peptide #1.
 KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amnial loss; nootropic;
 KW neuroprotective; antisense therapy; gene therapy.
 KW Synthetic.
 OS
 XX PN WO200150829-A2.
 PD 19-JUL-2001.
 XX PR 09-MAY-2001; 2001WO-1B00799.
 XX PR 09-MAY-2001; 2001WO-1B00799.
 XX PA (BIENKOWSKI M J.
 PA (GURNEY M E.
 PA (HEINRICKSON R L.
 PA (PARODI L A.

PA	(YANR/) YAN R;	XX	WPI; 2001-502549/55.
PI	Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;	XX	Novel purified polypeptide comprising fragment of mammalian aspartyl transmembrane domain and retaining beta secretase activity of Asp2 useful for identifying inhibitors of Asp2 activity
DR	WPI; 2001-483072/52.	XX	
PT	Novel purified polypeptide comprising fragment of mammalian aspartyl protease 2, lacking Asp2 transmembrane domain and retaining beta secretase activity -	XX	
PR	PT	XX	
PT	PT	XX	
PT	PT	XX	
PS	Example 12; Page 80; 185pp; English.	PS	Example 12; Page 80; 185pp; English.
XX	The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid precursor protein (APP) isoforms and their corresponding DNA molecules. Human aspartyl proteases can act as beta-secretase proteases useful for treating Alzheimer's disease. APP isoforms are useful for identifying modulators of amyloid-beta peptide production, for use in designing therapeutics for the treatment and prevention of Alzheimer's disease, dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. APP isoforms are also used in methods for identifying inhibitors and modulators of human Asp2 activity. The invention relates to a method for identifying agents that modulate the activity of human aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used as a means to screen in cellular assays for the inhibitors of beta- and gamma-secretase. Hu-Asp DNA fragments are useful as probes or primers in polymerase chain reactions (PCR). The probes are useful for detecting Hu-Asp nucleic acids in vitro assays and in Northern and Southern blots. The present sequence is a substrate peptide used to assay human aspartyl protease 2 (Asp-2) beta secretase activity.	XX	The invention relates to a purified polypeptide comprising a fragment of mammalian aspartyl protease (Asp2) protein which lacks the Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide and the fragment retain the beta-secretase activity of the mammalian Asp2 protein. The invention also details polynucleotides for the Asp2 protein. The invention relates to a polypeptide (isoform of APP) comprising the amino acid sequence of an APP cleavage site recognizable by a APP or its fragment containing an APP cleavage site comprising two lysine residues at the mammalian beta-secretase, and further comprising the mammalian APP or the carboxy terminus of the amino acid sequence of the mammalian APP or APP fragment. Also included in the invention are methods of identifying modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are useful for treating Alzheimer's disease. APP is useful in methods for identifying inhibitors or modulators of human Asp2 activity and therapeutic agents for the treatment or prevention of Alzheimer's disease. APP comprising the APP-Sw-beta-secretase peptide sequence (NLRA), which is associated with increased levels of Abeta processing is useful in assays relating the Alzheimer's research. The expression vector is useful for recombinantly expressing APP. Nucleic acids that hybridise to APP oligonucleotides are useful as probes or primers. The probes are useful for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and Southern blots. The present sequence is one of the products of Asp 2 degradation on the peptide sequence appearing as AAU6627.
SQ	Sequence 5 AA;	SQ	Sequence 5 AA;
Query	5 DAEFR 9	Query	5 DAEFR 9
Match	Score 5; DB 22; Length 5;	Match	Score 5; DB 22; Length 5;
Best Local Similarity	100.0%	Pred. No. 7.8e+05;	Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches	0;	Mismatches 0;	Mismatches 0;
Gaps	0;	Gaps 0;	Gaps 0;
Db	1 DAEFR 5	Db	1 DAEFR 5
RESULT 11		RESULT 12	
ID	AAU06636	ID	AAU07235
AC	AAU06636; XX	AC	AAU07235; XX
DT	24-OCT-2001 (first entry)	DT	24-OCT-2001 (first entry)
DE	Peptide product of Asp2 activity # 1.	DE	Human beta amyloid protein precursor, APP-beta secretase site peptide # 5.
XX	Aspartyl protease; Asp2; beta-secretase; nootropic; neuroprotective; amyloid-beta; Abeta.	XX	Human: aspartyl protease 1; Asp-1; nootropic; neuroprotective; APP-beta-secretase; Alzheimer's disease; APP-beta.
XX	Synthetic.	XX	Homo sapiens.
XX	XX	XX	KW Human: aspartyl protease 1; Asp-1; nootropic; neuroprotective; APP-beta-secretase; Alzheimer's disease; APP-beta.
XX	W0200149098-A2.	XX	KW KW
XX	09-MAY-2001; 2001WO-IB00798.	XX	KW KW
PD	12-JUL-2001.	PD	12-JUL-2001.
XX	PF 09-MAY-2001; 2001WO-IB00798.	PF 09-MAY-2001; 2001WO-IB00797.	XX
XX	XX	XX	PR 09-MAY-2001; 2001WO-IB00797.
PR	09-MAY-2001; 2001WO-IB00798.	PR	XX
XX	(BIEN/) BIENKOWSKI M J.	XX	PA (BIEN/) BIENKOWSKI M J.
PA	(HEIN/) HEINRIKSON R L.	PA (HEIN/) HEINRIKSON R L.	PA (GURN/) GURNEY M E.
PA	(PARO/) PARODI L A.	PA (PARO/) PARODI L A.	PA (YANR/) YAN R.
XX	BIenkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;	XX	PA (GURN/) GURNEY M E.
PI		PA	

PA	(HEIN/) HEINRIKSON R. L.	XX	(ELAN-) ELAN PHARM INC.
PA	(PARO/) PARODI L. A.	PA	
PA	(YANR/) YAN R.	XX	
XX		P1	Chrysler SMS, Sinha S, Keim PS, Anderson JP, Tan H, McConlogue LC;
PI	Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;	XX	
XX		DR	WPI; 2001-315578/33.
DR	Novel antibody that specifically binds native beta-secretase protein,	PT	
PT	useful for raising anti-idiotypic antibodies and for detecting or	PT	
PT	diagnosing pathological conditions related to presence of respective	PT	
PT	antigen	XX	
XX	Example; Column 28; 42PP; English.	PS	
PS		XX	
XX	The invention relates to a novel purified polypeptide comprising a fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide and the fragment retain the beta-secretase activity of the mammalian Asp2 protein. Also included is an isoform of anyloid protein precursor (APP) comprising the amino acid sequence of a APP or its fragment containing an APP cleavage site recognisable by a mammalian beta-secretase, and further comprising two lysine residues at the carboxy terminus of the amino acid sequence of the mammalian APP or APP fragment. The polypeptides are used for assaying for modulators of beta-secretase activity; identifying agents that inhibit the APP processing activity of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that modulate the activity of Asp2; and for reducing cellular production of amyloid beta (Abeta) from APP. Agents identified by the above methods are useful for treating Alzheimer's disease; and for identifying modulators of amyloid-beta (Abeta) peptide production, for use in designing therapeutics for the treatment or prevention of Alzheimer's disease. Probes and primers derived from Asp nucleic acid sequences are useful for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and Southern blots. The present sequence represents the amino acid sequence of human amyloid protein precursor, APP-beta secretase site peptide substrate #5 used in assays of human Asp2 beta-	CC	The sequences given in AAB47260-61 represent cleavage sites derived from wild-type and the Swedish mutation of beta-amyloid precursor protein (APP). These cleavage sites were used in fusion proteins which were used as substrates for the beta-secretase protein which is characterized by an ability to cleave the 695-amino acid isotype of APP between amino acids 596 and 597. The fusion proteins contain the carboxy-terminal end of Maltose binding protein (MBP) fused to the carboxy-terminal 125 amino acids of either wild type APP or APP containing the Swedish mutation. Beta-secretase is thought to be responsible for the pathogenic processing of APP to form beta-amyloid peptide (beta-AP) in beta-AP related conditions, e.g. Alzheimer's disease, Downs syndrome, HCHWA-D etc. Beta-secretase has a molecular weight of 260-300 kDa and will bind to wheat germ agglutinin but not to concanavalin A. Beta-secretase will cleave both the wild type and the Swedish mutation of APP.
XX	Sequence 5 AA;	SQ	CC
XX	Query Match 50.0%; Score 5; DB 22; Length 5;	Query Match	CC
XX	Best Local Similarity 100.0%; Pred. No. 7.8e+05;	Best Local Similarity	CC
XX	Matches 5; Conservative 0; Mismatches 0;	Matches	CC
XX	Indels 0; Gaps 0;	Indels	CC
XX	Sequence 5 AA;	Sequence	CC
XX		Qy	2 VPKMDA 6
XX		Db	1 VPKMDA 5
XX			
XX		RESULT 14	
XX		ABB0534	
XX		ID ABB06534 standard; Peptide; 5 AA.	
XX		XX	
XX		AC ABB0534;	
XX		DT 31-MAY-2002 (first entry)	
XX		DE Beta-secretase related peptide SEQ ID NO:129.	
XX		KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP; aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;	
XX		KW Alzheimer's disease.	
XX		XX	
XX		OS Homo sapiens.	
XX		OS Synthetic.	
XX		XX	
XX		PN WO2006306-A2.	
XX		XX	
XX		PD 24-JAN-2002.	
XX		XX	
XX		PP 19-JUL-2001; 2000US-219795P.	
XX		PR 12-MAR-2001; 2001US-275251P.	
XX		XX	
XX		PA (PHAA) PHARMACIA & UPTJOHN CO.	
XX		XX	
XX		PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;	
XX		PI Heinrikson RL;	
XX		DR WPI; 2002-216995/27.	

XX Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease -
 XX Disclosure; Page 166; 188pp; English.

XX The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC nootropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be used for
 CC manufacturing of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
 CC as a core structure to construct derivatives. ABL49925 and
 CC ABB06109 to ABB06593 represent sequences used in the exemplification
 CC of the present invention.

XX Sequence 5 AA;

Query Match 50.0%; Score 5; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KMDAE 7
 Db 1 KMDAE 5

RESULT 15

ABB06579
 ID ABB06579 standard; Peptide; 5 AA.
 XX
 AC ABB06579;
 XX DT 31-MAY-2002 (first entry)

XX DE Amyloid protein precursor peptide SEQ ID NO:180.
 XX KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
 KW Alzheimer's disease.
 XX OS Homo sapiens.
 OS Synthetic.
 PN WO200206306-A2.

XX PD 24-JAN-2002.
 XX PF 19-JUL-2001; 2001WO-US23035.
 XX PR 19-JUL-2000; 2000US-219795P.
 XX PR 12-MAR-2001; 2001US-27551P.
 XX PA (PHAA) PHARMACIA & UPJOHN CO.
 XX PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 PI Heinrikson RL;
 XX DR WPI; 2002-21695/27.

XX Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease -
 XX Example 8; Page 90; 188pp; English.
 XX The present invention describes an isolated peptide (I) comprising a

CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC nootropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be used for
 CC manufacturing of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
 CC as a core structure to construct derivatives. ABL49925 and
 CC ABB06109 to ABB06593 represent sequences used in the exemplification
 CC of the present invention.

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VKMDA 6
 Db 1 VKMDA 5

Search completed: April 21, 2003, 12:14:16
 Job time : 35 secs

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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:38:43 ; Search time 23.5 Seconds

(without alignments)
87,680 Million cell updates/sec

Title: US-09-580-018-10

Perfect score: 10
Sequence: 1 AEFRHDGWE 10

Scoring table: OUTGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 123

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database :

- 1: sp_archea;*
- 2: sp_bacteria;*
- 3: sp_fungi;*
- 4: sp_human;*
- 5: sp_invertebrate;*
- 6: sp_mammal;*
- 7: sp_mhc;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp Rodent;*
- 12: sp_virus;*
- 13: sp_vertebrate;*
- 14: spUnclassified;*
- 15: sp_virus;*
- 16: sp_bacteriap;*
- 17: sp_archeap;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	3	30.0	8	13	Q9PS69	Q9ps69 gallus gallus
2	3	30.0	10	6	Q9TJ33	Q9tj33 canis familiaris
3	3	30.0	10	10	P81899	P81899 prunus dulcis
4	3	30.0	10	12	Q91IGB	Q91igb tt virus, o
5	2	20.0	7	2	Q47477	Q47477 escherichia
6	2	20.0	7	4	Q15697	Q15697 homo sapiens
7	2	20.0	7	6	Q28742	Q28742 oryctolagus cuniculus
8	2	20.0	7	8	Q98666	Q98666 spinacia oleracea
9	2	20.0	8	2	Q68485	Q68485 kielmeyera
10	2	20.0	8	2	Q9XK1	Q9xk1 prochlorococcus
11	2	20.0	8	2	Q9SD5	Q9sd5 escherichia
12	2	20.0	8	2	P72221	P72221 pseudomonas
13	2	20.0	8	2	Q9RT2	Q9rt2 escherichia
14	2	20.0	8	2	Q9RR2	Q9rr2 shigella dysenteriae
15	2	20.0	8	2	Q9RXO	Q9rxo planktothrix
16	2	20.0	8	2	Q9RSL7	Q9rsl7 clostridium

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

[1]

RN SEQUENCE.

RP MEDLINE-92011685; PubMed=1918027;

RA Stifani S., Barber D.L., Aebersold R., Steyer E., Shen X., Nimpf J.,

RA Schneider W.J.;

RT receptor-related proteins; ";

RL J. Biol. Chem. 266:19079-19087(1991).

RT receptor-related proteins; "

FT NON_TER 1 1 1

FT SEQUENCE 8 AA; 846 MW;

SQ C007272DD865BAAA CRC64;

Query Match Score 3; DB 13; Length 8;

Best Local Similarity 100.0%; pred. No. 6.7e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DSG 8

Db 2 DSG 4

RESULT 2

ID Q9TU33

AC Q9TU33;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

RESULT 4
P81899 PRELIMINARY; PRT; 10 AA.
ID Q9JIG8 PRELIMINARY;
AC Q9JIG8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
RN 09JIG8;
RN 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
RN 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
RN ORF2.
RN TT virus.
RN OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
RN OC NCBITaxID=68887;
RN OC
RP SEQUENCE FROM N.A.
RX STRAIN=TIV-SM232;
RN [1]
RN SEQUENCE FROM N.A.
RN RC
RN MEDLINE=20251008; PubMed=10790123;
RN RX
RN NEI C.; Saback F.L.; Lampe E.;
RN "Coinfection with Multiple Tt Virus Strains Belonging to Different
RN Genotypes Is a Common Event in Brazilian Healthy Adults.";
RN RL J. Clin. Microbiol. 38:1926-1930 (2000).
RN DR EMBL AF216453; AAC F66899.1;
RN SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B5B9CB CRC64;
RN Query Match 30.0%; Score 3; DB 12; Length 10;
RN Best Local Similarity 100.0%; Pred. No. 3.3e-03;
RN Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AEF 3
Db 1 1 1
Db 2 AEF 4

RESULT 5
P81899 PRELIMINARY; PRT; 7 AA.
ID Q47477 PRELIMINARY;
AC Q47477;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
RN DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
RN DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
RN DE TP1 protein (fragment).
RN GN Escherichia coli.
RN OS Escherichia coli.
RN OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
RN OC Escherichia.
RN OX NCBITaxID=562;
RN RN [1]
RN RP SEQUENCE OF 7-7 FROM N.A.
RN RX MEDLINE=85203917; PubMed=3158524;
RN RA Hellings H.W.; Evans P.R.;
RN RT "Nucleotide sequence and high-level expression of the major
RN protein of Escherichia coli phosphofructokinase.";
RN RL Eur. J. Biochem. 149:363-373 (1985).
RN RN [2]
RN RP SEQUENCE FROM N.A.
RN RA Evans P.;
RN RL Submitted (Oct-1986) to the EMBL/GenBank/DBJ databases.
RN DR EMBL X02519; CAA26359.1;
RN FT NON_TER 1 1
RN SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;
RN Query Match 20.0%; Score 2; DB 2; Length 7;
RN Best Local Similarity 100.0%; Pred. No. 6.7e+05;
RN Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
P81899 PRELIMINARY; PRT; 7 AA.
ID Q15897 PRELIMINARY;
AC Q15897;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

RESULT 3
P81899 PRELIMINARY; PRT; 10 AA.
ID P81899 PRELIMINARY;
AC P81899;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Peptide-N-(N-acetyl-beta-D-glucosaminyl)asparagine amidase A, large
DE chain (Subunit A) (EC 3.5.1.52) (PGNase A) (Glycopeptide N-
DE glycosidase) (N-glycanase) (Fragment).
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
OC Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; Rosidae;
OC Rosids I; Rosales; Rosaceae; Amygdaloideae.
OX NCBI_TaxID=3755;
RN RN [1]
RN RP SEQUENCE AND CHARACTERIZATION.
RN RX PubMed=9543720;
RN RA Altmann F.; Paschinger K.; Dalik T.; Vorauer K.;
RN RT "Characterisation of peptide-N-(N-acetyl-beta-D-glucosaminyl)asparagine
RN amidase A and its N-glycans.";
RN RL Eur. J. Biochem. 252:118-123 (1998).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACEYL-D-
CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
CC CONTAINING AN ASPARTIC RESIDUE.
CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
CC -1- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
CC DEGLYCOSYLATION.
CC -1- MASS SPECTROMETRY: MW=54182; METHOD=WALDI-MS.
CC Hydrolase; Glycoprotein.
CC KW
CC NON_TER 10 1106 MW; 95F6BF65B1FB5865 CRC64;
CC SQ SEQUENCE 10 AA; 1106 MW; 95F6BF65B1FB5865 CRC64;
RN Query Match 30.0%; Score 3; DB 10; Length 10;
RN Best Local Similarity 100.0%; Pred. No. 3.3e-03;
RN Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SGY 9
Db 1 1
Db 3 SGY 5

DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophytina; Tracheophyta;
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	OC	Spermatophytina; Magnoliophytina; eudicots;
DE	(clone XP6A11A)	(Fragment).	OC	Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OS	Homo sapiens (Human).		NCBI_TAXID	3562;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		[1]	SEQUENCE FROM N.A.
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		RN	SEQUENCE FROM N.A.
OX	NCBI_TAXID=9606;		RX	MEDLINE=86120353; PubMed=3003688;
RN	RP	SEQUENCE FROM N.A.	RA	Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RC	TISSUE=PLACENTA;		RT	"Spinach plastid genes coding for initiation factor IF-1, ribosomal
RA	Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,		RT	protein S11 and RNA polymerase alpha-subunit.";
RA	Coombs M.I., Chiault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,		RL	Nucleic Acids Res. 14:1029-1044 (1986).
RA	Caskey C.T.H.;		DR	EMBL; X03496; CAA27215.1;
RA	"Isolation of chromosome-specific genes by reciprocal probing of		KW	Chloroplast.
RT	arrayed cDNAs and cosmid libraries.";		FT	NON_TER
RL	Hum. Mol. Genet. 0:0-0(1995).		SQ	SEQUENCE 7 AA; 907 MW;
DR	EMBL; L32077; ANA73887.1; -.		Query Match	644729D77409C420 CRC64;
FT	NON_TER		Best Local Similarity	20.0%; Score 2; DB 8; Length 7;
FT	NON_TER		Matches	100.0%; Pred. No. 6.7e+05; Mismatches 0; Indels 0; Gaps 0;
SQ	SEQUENCE 7 AA;		Qy	3 FR 4
DR	814 MW;		Db	2 FR 3
Qy	1 AE 2		RESULT 9	068485 PRELIMINARY; PRT; 8 AA.
Db	5 AE 6		ID	068485 ID 068485 PRELIMINARY; PRT; 8 AA.
Q28742	PRELIMINARY;		AC	068485; (TREMBLrel. 07, Created)
ID	Q28742	PRELIMINARY;	DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
AC	Q28742;	PRT; 7 AA.	DT	01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DT	01-NOV-1996	(TREMBLrel. 01, Created)	DE	Aminoglycoside 3'-O nucleotidyltransferase (Fragment).
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	GN	AA1A1
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	OS	Klebsiella pneumoniae.
DE	Alpha myosin heavy chain (Fragment).		Plasmid	PlQ1000.
OS	Oryctolagus cuniculus (Rabbit).		Bacteria	Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.		Klebsiella	Plasmid; Transferase.
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.		NCBI_TAXID	573;
RN	[1]		RN	SPRAINS-K1;
RP	SEQUENCE FROM N.A.		RC	SUPRAINS-K1;
Q28742	PRELIMINARY;		RX	MEDLINE=98287600; PubMed=9624504;
ID	Q28742	PRELIMINARY;	RA	"Characterization of the 6'-N-aminoglycoside acetyltransferase gene
AC	Q28742;	PRT; 7 AA.	Centron D.", Roy P.H.;	act(6')-Iq from the integron of a natural multiresistance plasmid."
DT	01-NOV-1996	(TREMBLrel. 01, Created)	RT	RT
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	RL	Antimicrob. Agents Chemother. 42:1506-1508 (1998).
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	DR	EMBL; AF047556; AAC25501.1; -.
DE	Alpha myosin heavy chain (Fragment).		KW	Plasmid; Transferase.
OS	Oryctolagus cuniculus (Rabbit).		FT	NON_TER
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.		SQ	SEQUENCE 8 AA; 878 MW;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.		EFC1B5A2CB1DD0056 CRC64;	EFC1B5A2CB1DD0056 CRC64;
RN	[1]		Query Match	20.0%; Score 2; DB 2; Length 8;
RP	SEQUENCE FROM N.A.		Best Local Similarity	100.0%; Pred. No. 6.7e+05; Mismatches 0; Indels 0; Gaps 0;
RX	MEDLINE=801221301; PubMed=6328491;		Qy	1 AE 2
RA	Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovicic S.,		Db	1 AE 4
RA	Rabinowitz M.;		3 AE 4	
RT	"Characterization of genomic clones specifying rabbit alpha- and beta-			
RT	ventricular myosin heavy chains";			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).			
DR	EMBL; K01698; AAA31415.1; -.			
FT	NON_TER			
SQ	SEQUENCE 7 AA;			
DR	916 MW;			
Qy	5 HD 6			
Db	4 HD 5			
RESULT 8	Q9X3K1	PRELIMINARY;	PRT;	8 AA.
098866	PRELIMINARY;	PRT;	7 AA.	
ID	098866	PRELIMINARY;	AC	Q9X3K1;
AC	098866-1999	(TREMBLrel. 10, Created)	DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DT	01-MAY-1999	(TREMBLrel. 10, Last annotation update)	DE	Cytochrome b (Fragment).
DE	Cytochrome b/f subunit IV (Fragment).		GN	BETB.
OS	Spinacia oleracea (Spinach).		OS	Prochlorococcus sp.
OC	Chloroplast.		OC	Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;

OX	NCBI_TaxID=1220;		RC	STRAIN=OS-AUG-9;
RN	[1] SEQUENCE FROM N.A.		RX	MEDLINE=9339366; PubMed=8336113;
RP			RA	Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
RA	Urbach E., Chisholm S.W.;		RT	"Cloning, sequence analysis and expression in Escherichia coli of a
RA	"Genetic diversity in Prochlorococcus populations flow cytometrically		RT	gene encoding an algalinate lyase from Pseudomonas sp. OS-ALG-9.";
RT	sorted from the Sargasso Sea and Gulf Stream.";		RL	J. Gen. Microbiol. 139:987-993(1993).
RT	Limonol. Oceanogr. 43:1615-1630(1998).		DR	EMBL; D38469; BAA21704.1; -.
RL			KW	Lyase.
DR			FT	FT NON_TER 1 1
FT	AAD23233.1; -.		FT	NON_TER 8 8
NON_TER	1 1		SEQUENCE 8 AA;	841 MW; 461DDDC5A5B041BB CRC64;
SQ				
Query Match	20.0%; Score 2; DB 2; Length 8;		Query Match	20.0%; Score 2; DB 2; Length 8;
Best Local Similarity	100.0%; Pred. No. 6.7e+05;		Best Local Similarity	100.0%; Pred. No. 6.7e+05;
Matches	2; Conservative 0; Mismatches 0; Indels 0;		Matches	2; Conservative 0; Mismatches 0; Indels 0;
Qy	7 SG 8		Qy	1 AE 2
	1 1			1 1
Db	5 SG 6		Db	7 AE 8
RESULT 11			RESULT 13	
O9S6D5	PRELIMINARY;	PRT;	O9R7T2	PRELIMINARY;
ID	O9S6D5;		ID	O9R7T2;
AC			AC	O9R7T2;
DT	01-MAY-2000 (TREMBLrel. 13, Created)		DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)		DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Putative IS01 transposase (Fragment).		DE	Hypothetical 1.0 kDa protein (Fragment).
OS	Escherichia coli.		GN	YORG.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		OS	Escherichia coli.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		OC	Escherichia.
NCBI_TaxID=562;			NCBI_TaxID=562;	
RN	[1]		RN	[1]
SEQUENCE FROM N.A.			SEQUENCE FROM N.A.	
RX	STRAIN=A295B;		RC	STRAIN=K12;
MDLINB=99194747; PubMed=10094716;			RX	MEDLINE=97061202; PubMed=8905232;
Rahn A., Drummondsmith J., Whitfield C.;			RA	Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RT	"Conservation in the cps gene clusters for expression of		RA	Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RT	Escherichia coli group 1 K antigens: relationship to the colanic acid		RA	Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RT	biosynthesis locus and the cps genes from Klebsiella pneumoniae.";		RA	Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RT	J. Bacteriol. 181:2307-2313(1999).		RA	Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
DR	EMBL; AFL18251; AAD30008.1; -.		RA	Yano M., Horikuchi T.;
DR			RT	"A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
FT	NON_TER 8 8		RT	to the 12.7-28.0 min Region on the Linkage Map.";
SQ	SEQUENCE 8 AA;	1011 MW;	FT	RL DNA Res. 3:137-155(1996).
Query Match	20.0%; Score 2; DB 2; Length 8;		DR	D90705; BAA35310.1; -.
Best Local Similarity	100.0%; Pred. No. 6.7e+05;		KW	Hypothetical protein.
Matches	2; Conservative 0; Mismatches 0; Indels 0;		FT	NON_TER 1 1
Qy	1 AE 2		SQ	SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A_CRC64;
	1 1		Query Match	20.0%; Score 2; DB 2; Length 8;
Db	7 AE 8		Best Local Similarity	100.0%; Pred. No. 6.7e+05;
			Matches	2; Conservative 0; Mismatches 0; Indels 0;
RESULT 12			Q9R5R2	PRELIMINARY;
P72221	PRELIMINARY;	PRT;	ID	Q9R5R2;
ID	P72221;		AC	Q9R5R2;
AC	P72221;		AC	Q9R5R2;
DT	01-FEB-1997 (TREMBLrel. 02, Created)		DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)		DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Alignate lyase (Fragment).		DE	31,000 DA product of ORF8 (Fragment).
GN	Pseudomonas sp. (strain OS-ALG-9).		OS	Shigella dysenteriae.
OS	Bacteria; Proteobacteria.		OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
NCBI_TaxID=86038;			OC	Shigella.
RN	[1]		NCBI_TaxID=622;	
RP	SEQUENCE FROM N.A.			
RC	STRAIN=OS-ALG-9;			
RA	Submitted (Oct-1994) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			

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RN      [1]
RP      SEQUENCE.
RX      MEDLINE-92085268; PubMed=1660923;
RA      Pollard P., Prete M.F., Chandler M., Fayet O.;
RT      "Programmed translational frameshifting and initiation at an AUU codon
       in gene expression of bacterial insertion sequence IS911." ;
RL      J. Mol. Biol. 222:465-477(1991).
FT      NON_TER 8 8
SQ      SEQUENCE 8 AA; 902 MW; FE2DCAFB86AE336 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      8 GY 9
          |||
Db      4 GY 5

RESULT 15
Q9R3X0  PRELIMINARY;   PRT;    8 AA.
ID      Q9R3X0;
AC      Q9R3X0;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE      Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
DE      (Fragment).
GN      RBLN.
OS      Planktothrix rubescens.
OC      Bacteria; Cyanobacteria; Oscillatiales; Planktothrix.
OX      NCBI_TaxID=59512;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BC-PLA 9316, AND BC-PLA 9303;
RX      MEDLINE=20005589; PubMed=10537197;
RA      Beard S.J., Handley B.A., Hayes P.K., Walsby A.E. ;
RT      "The diversity of gas vesicle genes in Planktothrix rubescens from
       Lake Zurich." ;
RL      Microbiology 145:2757-2768(1999).
DR      EMBL; AJ132249; CAB59537.1;
DR      EMBL; AJ132248; CAB59534.1;
FT      NON_TER 1 1
SQ      SEQUENCE 8 AA; 957 MW; 33D1AA685BB19CB CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      2 EF 3
          |||
Db      1 EF 2

```

Search completed: April 21, 2003, 12:41:58
 Job time : 23.5 secs



peptide-N-(N-acetyl-beta-D-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain N; Alternative names: Peptidase N-glycosidase C; Species: Prunus dulcis var. sativa (sweet almond) C; Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000 R; Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K. Bur. J. Blochem. 252, 118-123, 1998 A; Title: Characterisation of Peptide-N4-(N-acetyl-beta-D-glucosaminyl)asparagine amidase A; Accession number: A59272; MUID:9818894; PMID:9523720 A; Reference number: PH0891; PMID:1836012 A; Accession: A59272 A; Status: preliminary A; Molecule type: protein A; Residues: 1-10 <AM> C; Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	7	SGY 9
Db	3	SGY 5

RESULT 6
PT0090 T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0900
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbergk, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allel A; Reference number: PH0891; PMID:92078857; MUID:1836012
A; Accession: PH0900
A; Molecule type: mRNA
A; Residues: 1-10 <GOL>
A; Experimental source: myelin basic protein-immunized T-cell
C;Keywords: T-cell receptor

Query Match 30.0%; Score 3; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6	DSG 8
Db	5	DSG 7

RESULT 7
A41225 copper resistance protein A - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: A41225
R;Cha, J.S.; Cooke, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane protein A; Accession number: A41225; MUID:92020961; PMID:1924351
A; Accession: A41225
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-5 <CHA>

Query Match 20.0%; Score 2; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	7	SG 8
Db	2	SG 3

RESULT 8
A41225 copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: B41225
R;Cha, J.S.; Cooke, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane protein A; Accession number: A41225; MUID:92020961; PMID:1924351
A; Accession: B41225
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-5 <CHA>

Query Match 20.0%; Score 2; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AE 2
Db	1	AE 2

RESULT 9
D60274 major protein antigen MPT46 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: D60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kiyomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the culture
A;Reference number: A60274; PMID:9109989; MUID:1698899
A;Accession: D60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <MGR>

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DS 7
Db 1 |
Db 2 DS 3

RESULT 10
B37988 acid Proteinase light chain - slime mold (*Physarum polycephalum*) (fragment)
C;Species: *Physarum polycephalum*
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C;Accession: B37988
R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Ogata; Biol. Chem. 265, 19998-19903, 1990
A;Title: Purification and characterization of a novel intracellular acid proteinase from *Physarum polycephalum*
A;Reference number: A37988; PMID:9106608; MUID:2246266
A;Accession: B37988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <MUR>

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
Db 1 |
Db 1 AE 2

RESULT 11
A44692 fulicin - giant African snail
C;Species: *Achatina fulica* (giant African snail)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C;Accession: A44692
R;Ohca, N.; Kubota, I.; Takao, T.; Shimomishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; NC Biochem. Biophys. Res. Commun. 178, 486-493, 1991
A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t A;Reference number: A44692; MUID:91313471; PMID:1859408
A;Accession: A44692
A;Molecule type: protein
A;Residues: 1-5 <OHN>
C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide F; 2' Modified site: D-asparagine (Asn) #status experimental
F; 5' Modified site: amidated carboxyl end (Val) #status experimental

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EF 3
Db 1 |
Db 3 EF 4

RESULT 12
JTF0520 Ig kappa chain V-III region (SD1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Aug-1996
C;Accession: JTF0520
R;Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A;Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A;Reference number: JTF0511; MUID:89279157; PMID:2786547
A;Accession: JTF0520
A;Molecule type: mRNA
A;Residues: 1-5 <ANK>
A;Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
A;Note: a stop codon terminates the sequence in the V region
C;Keywords: heterotetramer; immunoglobulin
F; 1-5/Domain: V kappa region <PRE>

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8
Db 1 |
Db 3 SG 4

RESULT 13
D44823 synaptosomal-associated protein SNAP-25 peptide 2 - rabbit (fragment)
N;Alternate name: synaptosomal-associated protein peptide 2
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: D44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein)
A;Reference number: A44823; MUID:92044785; PMID:1941090
A;Accession: D44823
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <LOE>
A;Experimental source: visual tissue
A;Role: sequence extracted from NCB1 backbone (NCBIP:64250)
C;Keywords: membrane trafficking

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SG 8
Db 1 |
Db 4 SG 5

RESULT 14
PT0513 T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0513; PR0606
R;Feeley, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PR0513
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <PFE>
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AL
A;Accession: PR0606
A;Status: translation not shown

A; Molecule type: mRNA
A; Residues: 1-5 <FE2>
C; Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 SG B
 |
Db 2 SG 3

RESULT 15
PT0600
T-cell receptor beta chain V-D-J region (120-1C) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991.
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; PMID:91277601; PMID:1711558
A; Accession: PT0600
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-5 <FE2>
A; Experimental source: newborn thymus, strain BALB/c
C; Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 DS 7
 |
Db 4 DS 5

Search completed: April 21, 2003, 12:42:31
Job time : 14 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	2	PRED_40:	2	20.0	5	1 RE21_LITRU
2	2		2	20.0	5	1 RE31_LITRU
3	2		3	20.0	5	1 UXA4_CHTR
4	2		4	20.0	6	1 FARP_MONEX
5	2		5	20.0	6	1 TRP_LPSEPU
6	2		6	20.0	6	1 UN05_CLOPA
7	2		7	20.0	7	1 EI05_LITRU
8	2		8	20.0	7	1 FAR1_ASCSU
9	2		9	20.0	7	1 UF03_MSCSU
10	2		10	20.0	8	1 AL17_CARMA
11	2		11	20.0	8	1 ALL5_CYDPO
12	2		12	20.0	8	1 CPDI_EENTFA
13	2		13	20.0	8	1 GLUR_HUMAN
14	2		14	20.0	8	1 LCK5_LEUMA
15	2		15	20.0	8	1 PPK3_PERAM
16	2		16	20.0	8	1 UC26_MAIZE
17	2		17	20.0	8	1 VGLG_HSV2B
18	2		18	20.0	9	1 COXO_THUOB
19	2		19	20.0	9	1 DS11_RABIT
20	2		20	20.0	9	1 FAR5_ASCSU
21	2		21	20.0	9	1 FAR6_CALVO
22	2		22	20.0	9	1 FARP_CALST
23	2		23	20.0	9	1 FIBB_MACFU
24	2		24	20.0	9	1 FIBB_PAPAN
25	2		25	20.0	9	1 MOSF_CLVJA
26	2		26	20.0	9	1 MOSH_CLVJA
27	2		27	20.0	9	1 NEUU_CAVFO
28	2		28	20.0	9	1 NEUX_HUMAN
29	2		29	20.0	9	1 OXYT_OCTVU
30	2		30	20.0	9	1 TKL1_LOOMI
31	2		31	20.0	9	1 TRP1_LEOMA
32	2		32	20.0	9	1 XYLA_STRSQ
33	2		33	20.0	10	1 COXO_RAT

SEQUENCE AND MASS SPECTROMETRY.						
SEQUENCE=Skin secretion;						
RC TISSUE=Skin secretion;						
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,						
Tyler M.J., Wallace J.C.,						
RA						
RN						
SEQUENCE, AND MASS SPECTROMETRY.						
SEQUENCE=Skin secretion;						
RC TISSUE=Skin secretion;						
RA						
RT						
"The structure of new peptides from the Australian red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians."						
RT						
RL Aust. J. Chem. 49:955-963(1996).						
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBOTIC ACTIVITY.						
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.						
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.						
KW Amphibian skin,						
SEQUENCE 5 AA: 626 MW: 6DD9C9CB1030000 CRC64;						
Query Match Score 2; DB 1; Length 5;						
Best Local Similarity 100.0%; Fred. No. 1.1e+05;						
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY 2 EF 3						
RE31_LITRU STANDARD; PRT; 5 AA.						
ID RE31_LITRU						
AC PB2072; Created)						
DT 15-JUN-2002 (Rel. 41, Last sequence update)						
DE Rubellidin 3.1;						
OS Litoria rubella (Desert tree frog)						
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;						
OC Peledrydinidae; Litoria.						
OX NCBI_TaxID=104895;						
RN SEQUENCE, AND MASS SPECTROMETRY.						
SEQUENCE=Skin secretion;						
RC TISSUE=Skin secretion;						
RA						
RT						
"The structure of new peptides from the Australian red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians."						
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"The structure of new peptides from the Australian red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians."						
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"The structure of new peptides from the Australian red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians."						

RT "The structure of new peptides from the Australin red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians." ;
 RT Aust. J. Chem. 49:955-967(1996).
 -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
 CC Amphibian skin; Amidation.
 KW MOD_RES 5 5 AMIDATION.
 FT MOD_RES 5 AM; 656 MW; 71A9C9CB10300000 CRC64;
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;
 Query Match Score 20.0%; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EF 3
 Db 2 EF 3

RESULT 3
 UXA4_CHLTR ID UXA4_CHLTR STANDARD; PRT; 5 AA.
 AC P38005; DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elemental body (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 RN [1]
 RP SEQUENCE.
 STRAIN=L2/434/Bu;
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M., Comanducci M., Christianen G., Birellund S., Vretou E., Ratti G., RA Pallini V.;
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.5; ITS MW IS: 28 kDa.
 DR Stena-2DPAGE; P38005; -.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;
 Query Match Score 20.0%; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8
 Db 2 SG 3

RESULT 4
 FARP_MONEX ID FARP_MONEX STANDARD; PRT; 6 AA.
 AC P41966; DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FMRFamide-like neuropeptide GNFRFR-amide.
 OS Moniezia expansa (Sheep tapeworm).
 OC Cyclopophyllidae; Metazoa; Platyhelminthes; Cestoda; Eucestoda; OC Anoplocephalidae; Moniezia.
 OX NCBI_TAXID=28841;
 RN SEQUENCE.
 RX MEDLINE=93312289; PubMed=8323531;
 RA Matile A.G., Shaw C., Halton D.W., Thim L.;
 RT "GNFRFamide: a novel FMRFamide-immunoreactive peptide isolated from the sheep tapeworm, *Moniezia expansa*";
 RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 6 6 AMIDATION.
 FT SEQUENCE 6 AA; 787 MW; 69d049c9c4481000 CRC64;
 SQ Query Match Score 20.0%; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FR 4
 Db 4 FR 5

RESULT 5
 TRP_PSEPU ID TRPL_PSEPU STANDARD; PRT; 6 AA.
 AC P36414; DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TRPBA operon transcriptional activator (Fragment).
 GN TRP1.
 OS Pseudomonas putida
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG1 C1S;
 RX MEDLINE=8933826; PubMed=2503057;
 RA Eberly L., Crawford I.P.;
 RT "DNA sequence of the tryptophan synthase genes of *Pseudomonas putida*."
 RT Biochimie 71:521-531(1989).
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE TRPAB OPERON, OVERLAPPING ITS OWN PROMOTOR REGION.
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; X13299; CAR31660.1;
 DR InterPro; IPR000844; HTH_LYSR_FAMILY; PARTIAL.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.
 KW Tryptophan biosynthesis; Transcription regulation; Activator;
 KW DNA-binding.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1E6DD6F000 CRC64;
 Query Match Score 20.0%; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 HD 6
 Db 3 HD 4

RESULT 6
 UN06_CLOPA ID UN06_CLOPA STANDARD; PRT; 6 AA.
 AC P81351;
 DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 6 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TAXID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=96291870; PubMed=9629918;
 RA Flengsrød R.; Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806 (1998).
 CC ~1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AE 2
 Db 4 AE 5

RESULT 7
 EI05_LITRU STANDARD; PRT; 7 AA.
 ID EI05_LITRU
 AC P82101;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Electrin 5.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
 OC Pelodyadinae; Litoria; Litoria.
 OX NCBI_TAXID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645 (1999).
 CC ~1- SUBCELLULAR LOCATION: SECRETED.
 KW Amphibian skin; Amidation.
 FT MOD_RES 7 7
 SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 YE 10
 Db 2 YE 3

RESULT 8
 FARI_ASCSU STANDARD; PRT; 7 AA.
 ID FARI_ASCSU
 AC P31889;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuropeptide AFL.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TAXID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90180465; PubMed=2627377;
 RA Cowden C., Stretton A.O.W., Davis R.E.;
 RT "AFL, a sequenced bioactive neuropeptide isolated from the nematode
 Ascaris suum";
 RT Ascaris suum.";
 RL Neuron 2:1165-1473 (1989).
 CC -!- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTORNEURONS. REDUCES THE
 INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
 CELLS.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
 GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 7
 SQ SEQUENCE 7 AA; 953 MW; 69A04059CB144350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EF 3
 Db 3 EF 4

RESULT 9
 UF03_MOUSE STANDARD; PRT; 7 AA.
 ID UF03_MOUSE
 AC P38641;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DT Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus;
 OX NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=FBibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familiar and novel murine proteins
 using preparative two-dimensional gel electrophoresis.",
 RT Electrophoresis 15:735-745 (1994).
 RL -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DBB1B1180 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
 Db 4 AE 5

RESULT 10
 AL17_CARMA STANDARD; PRT; 8 AA.
 ID AL17_CARMA
 AC PB820;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 17.
 OS Carcinus maenas (Common shore crab) (Green crab).

OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;	OX	NCBI_TAXID=1351;
OC	Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;	RN	[1]
OC	Brachyura; Brachyura; Portunidae; Portunidae; Carcinus.	RP	SEQUENCE.
OX	[1]	SEQUENCE.	
RN		SEQUENCE.	
RC	TISSUE="cerebral ganglion, and thoracic ganglion;	RA	MEDLINE=85040388; PubMed=5436978;
RA	Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.; "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab <i>Carcinus maenas</i> .";	RA	Suzuki A., Mori M., Saigaki Y., Isogai A., Fujino M., Kitada C., Craig R.A., Clewell D.B.;
RA	Eur. J. Biochem. 250:727-734 (1997).	RA	"Isolation and structure of bacterial sex pheromone, CPD1."
RL	-1- SIMILARITY: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.	RT	Science 226:843-850 (1984).
CC	-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.	CC	-1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE BACTERIOCIN PLASMID PPD1.
CC	Neuropeptide; Amidation; Multigene family.	CC	
FT	MOD_RES 8 8 AMIDATION (POTENTIAL).	CC	
SEQUENCE 8 AA;	858 MW; C82879D5AB46D865 CRC64;	SQ	SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;
Query Match	20.0%; Score 2; DB 1; Length 8;	Qy	Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	7 SG 8	RESULT 13	Query Match 20.0%; Score 2; DB 1; Length 8;
Db	1 SG 2	GLUR_HUMAN	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
		ID GLUR_HUMAN	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		STANDARD;	
		PRT;	
		PTT;	8 AA.
RESULTS 11			
ALL5_CYDPO			
ID ALL5_CYDPO			
AC P82156;			
DT 30-MAY-2000 (Rel. 39, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			
DE Cydiastatin 5.			
OS Cydia pomonella (Codling moth).			
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Diptera; Tortricoidea; Tortricidae; Olethreutinae; Cydia.			
NCBI_TAXID=82600;			
RN [1]			
RP			
RC TISSUE=larva;			
RX MEDLINE=9804539; PubMed=9392829;			
RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winsstanley D., Dave M., East P.D., Thorpe A.;			
RT "Lepidopteran peptides of the allatostatin superfamily.";			
RL Peptides 18:1301-1309 (1997).			
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.			
KW Neuropeptide; Amidation.			
FT MOD_RES 8 8 AMIDATION.			
SEQUENCE 8 AA;	898 MW; 922879CABB58640D CRC64;	Qy	Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	8 GX 9	RESULT 14	Query Match 20.0%; Score 2; DB 1; Length 8;
Db	1 3 GX 4	LCK5_LEUMA	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
		ID LCK5 LEUMA	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		STANDARD;	
		PRT;	
		PTT;	8 AA.
RESULTS 12			
CPD1_ENTFA			
ID CPD1_ENTFA			
AC P13269;			
DT 01-JAN-1990 (Rel. 13, Created)			
DT 01-JAN-1990 (Rel. 13, Last sequence update)			
DT 01-FEB-1991 (Rel. 13, Last annotation update)			
DE Sex pheromone CPD1.			
OS Enterococcus faecalis (Streptococcus faecalis).			
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.			
OC Blaberoidea; Blaberidae; Leucophaea.			
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Mandibulata; Pancrustacea; Hexapoda; Archipoda; Blattaria.			
OC Blaberoidea; Blaberidae; Leucophaea.			
OX NCBI_TAXID=6388;			
RN [1]			

RP
 SEQUENCE.
 RC TISSUE=Head;
 RX MEDLINE=87052651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic peptides of Leucophæa maderae.";
 RT Comp. Biochem. Physiol. 88C:27-50(1987).
 CC -1- FUNCTION: THIS CEPHALOMYOOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 DR PIR: JS0315; JS0315.
 KW Neuropeptide; Amidation.
 MOD RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 784 MW; 73636A5B3C865B8 CRC64;

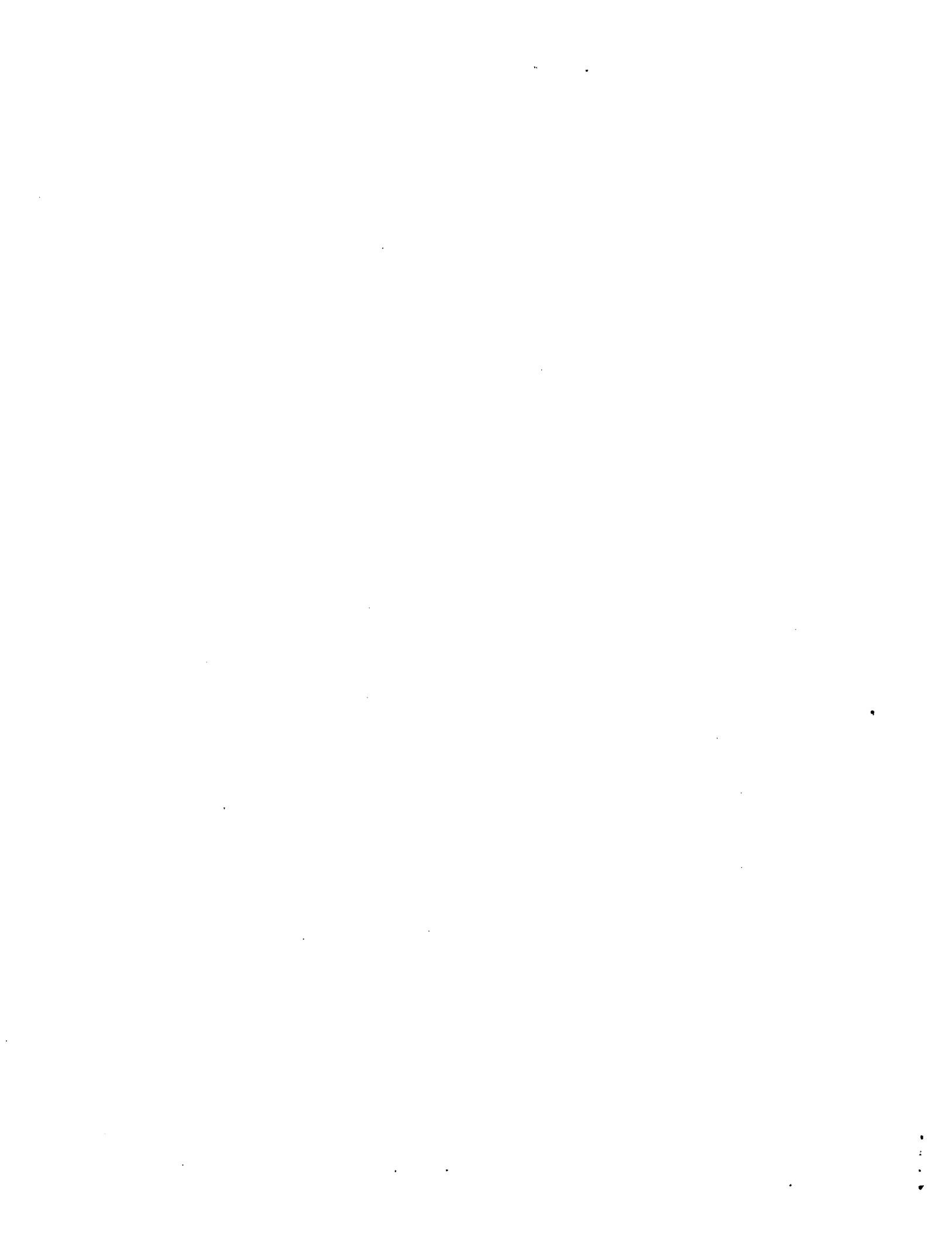
Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SG 8	Db 2 SG 3
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RESULT 15
 PPK3_PERAM STANDARD PRT; 8 AA.
 ID_PPK3_PERAM
 AC P82618;
 DT 16-OCT-2001 (Rel. 4.0, Created)
 DT 16-OCT-2001 (Rel. 4.0, Last sequence update)
 DE Pyrokinin-3 (Rel. 4.0, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPPU-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattoidea; Blattidae; Periplaneta.
 NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196716;
 RA Predeel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144 (1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=2018894; PubMed=10723010;
 RA Predeel R., Eckert M.;
 RT "Tissue-specific distribution of FXPPRlamides in the nervous system of the American cockroach";
 RT J. Comp. Neurol. 419:352-363 (2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
 CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 MOD RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 997 MW; OB341740D772C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FR 4	Db 4 FR 5
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DOCUMENTS

RESULT 1	
AAB46214	
ID	AAB46214 standard; peptide; 10 AA.
XX	
AC	AAB46214;
XX	
DT	04-APR-2001 (first entry)
XX	
DE	Human APP derived immunogenic peptide #10.
XX	
KW	Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW	FC receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW	amyloid precursor protein Alzheimer's disease

score greater than or equal to the score of the result to have a chance to be printed, and is derived by analysis of the total score distribution.

סבצ'ה

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	22	AAB6214 Human APP derived
2	9	90.0	10	15	AAR8928 Human amyloid precursor protein
3	9	90.0	10	22	AAB6213 Human APP derived
4	9	90.0	10	22	AAB6215 Human APP derived
5	8	80.0	10	22	AAB6212 Human APP derived
6	8	80.0	10	22	AAB6216 Human APP derived
7	7	70.0	8	23	AAU78518 N terminus of beta-amyloid protein
8	7	70.0	10	22	AAB6211 Human APP derived
9	7	70.0	10	22	AAB6217 Human APP A-beta
10	6	60.0	7	22	AAB6202 Human APP A-beta

07-DEC-2000; 26-MAY-2000; 28-MAY-1999; 2000WO-US14810
99US-032228

XX PA (NEUR-) NEURALAB LTD.
XX PA
XX PT
XX P I Schenk DB, Bard F, Vassquez NJ, Yednock T;
XX DR WPI; 2001-032104/04.
XX PT Preventing or treating a disease associated w/
XX PR especially Alzheimer's disease, comprises admin-
XX PR spective, antibiotic,
XX PR

XX Disclosure; Figure 19; 143pp; English.
 PS
 XX This invention describes a novel method of preventing or treating a disease associated with amyloid deposits of amyloid precursor protein (APP) Abeta fragments in the brain of a patient, which comprises a antibody binds to an amyloid protein and induces a clearing response (Fc receptor mediated phagocytosis) against it (b) a polypeptide containing an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent that induces an immunogenic response against residues 1-3 to 7-11 of Abeta. The products of the invention have nontropic and neuroprotective activity. The method is also useful for monitoring a course of treatment being administered to a patient e.g. active and passive immunization. The methods are useful for prophylactic and therapeutic treatment of Alzheimer's disease.

XX Sequence 10 AA:
 SQ Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ID AAR58928 standard; peptide; 10 AA.
 QY 1 AEFRHDSGY 10
 DB 1 AEFRHDSGY 10

RESULT 2
 AAR58928
 ID AAR58928 standard; peptide; 10 AA.
 XX AC AAR58928;
 XX DT 15-APR-1995 (first entry)
 XX DE Human amyloid precursor protein APP695 residues 597-606.
 XX KW Amyloid precursor protein; isoform APP 695; beta amyloid; Alzheimer's disease.
 XX OS Homo sapiens.
 PN WO9419692-A.
 XX PD 01-SEP-1994.
 XX PF 17-FEB-1994; 94WO-US01712.
 XX PR 18-FEB-1993; 93US-0019208.
 XX PA (GENO) GEN HOSPITAL CORP.
 XX PI Nishimoto I;
 XX DR 1994-294486/36.
 XX WPI: 1994-294486/36.

PT Identifying cnds. useful for treating or preventing Alzheimer's disease - by determining whether it interferes with the association of the coupline portion of amyloid precursor protein to G polypeptide
 PT to G polypeptide
 XX Disclosure; Page 33; 71pp; English.

PS Beta amyloid is synthesised as part of a larger protein referred to in humans, including APP695 and APP770. The amino terminal of beta amyloid is generated by cleavage of a peptide bond of APP which in APP595 lies between Met596 and Asp597. APP forms a complex with Go, a GTP-binding protein (or "G protein") in brain. Go is made of one alpha subunit and one Beta-gamma subunit. Two isoforms of Go, known as Go1 (or Go) and Go2 (or GoB) have been identified; they have slight AA differences in their alpha subunits. The cDNA sequence and

CC deduced AA sequence of the alpha subunits in each of Go1 and Go2 are shown in AAQ69002/R58914 and AAQ69004/R58924 respectively. The CC cytoplasmic APP695 sequence Hs657-lys676 (AAR58913) possesses a specific Go-activating function, and is necessary for complex CC formation of this APP with Go. AAR58928 is another peptide of CC APP695 which correponds to AAS 597-606.
 CC SQ Sequence 10 AA:
 CC Query Match 90.0%; Score 9; DB 15; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 0.00049; Mismatches 0; Indels 0; Gaps 0;
 CC XX QY 1 AEFRHDSGY 9
 CC DB 2 AEFRHDSGY 10

RESULT 3
 AAB46213
 ID AAB46213 standard; peptide; 10 AA.
 XX AC AAB46213;
 XX DT 04-APR-2001 (first entry)
 XX DE Human APP derived immunogenic peptide #9.
 XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nontropic; FC receptor mediated phagocytosis; immunogenic response; neuroprotective; amyloid precursor protein; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO2000072880-A2.
 XX PD 07-DEC-2000.
 XX PR 26-MAY-2000; 2000WO-US14810.
 XX PA (NEUR-) NEURALAB LTD
 XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX DR WPI; 2001-032104/04.
 XX PT Preventing or treating a disease associated with amyloid deposits, especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a disease associated with amyloid deposits of amyloid precursor protein (APP) Abeta fragments in the brain of a patient, which comprises a antibody binds to an amyloid deposit and induces a clearing response (FC receptor mediated phagocytosis) against it (b) a polypeptide containing an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent that induces an immunogenic response against residues 1-3 to 7-11 of Abeta. The products of the invention have nontropic and neuroprotective activity. The method is also useful for monitoring a course of treatment being administered to a patient e.g. active and passive immunization. The methods are useful for prophylactic and therapeutic treatment of Alzheimer's disease.
 XX SQ Sequence 10 AA:
 CC Query Match 90.0%; Score 9; DB 22; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 0.00049; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AEFRHDSGY 9 	DT 04-APR-2001 (first entry)
Db	2 AEFRHDSGY 10	XX Human APP derived immunogenic peptide #8.
RESULT 4		XX Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
ID AAB46215		KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;
ID AAB46215 standard; peptide; 10 AA.		KW amyloid precursor protein; Alzheimer's disease.
XX		XX Homo sapiens.
AC AAB46215;		OS
XX		XX
DT 04-APR-2001 (first entry)		PN WO200072880-A2.
XX		XX
DE Human APP derived immunogenic peptide #11.		PD 07-DEC-2000.
XX		XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;		PF 26-MAY-2000; 2000WO-US14810.
KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;		XX
KW amyloid precursor protein; Alzheimer's disease.		PR 28-MAY-1999; 99US-0322289.
XX		XX
OS Homo sapiens.		PA (NEUR-) NEURALAB LTD.
XX		XX
Pi Schenk DB, Bard F, Vasquez NJ, Yednock T;		PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX		XX
PN WO200072880-A2.		DR WPI; 2001-032104/04.
XX		XX
PD 07-DEC-2000.		PT Preventing or treating a disease associated with amyloid deposits,
XX		PT especially Alzheimer's disease, comprises administering amyloid
PF 26-MAY-2000; 2000WO-US14810.		PT specific antibody
XX		XX
PR 28-MAY-1999; 99US-0322289.		PS Disclosure; Figure 19; 143pp; English.
XX		XX
PA (NEUR-) NEURALAB LTD.		CC This invention describes a novel method of preventing or treating a
XX		CC disease associated with amyloid deposits of amyloid precursor protein
Pi Schenk DB, Bard F, Vasquez NJ, Yednock T;		CC (APP) Abeta fragments in the brain of a patient, which comprises
XX		CC (APP) Abeta fragments in the brain of a patient, which comprises
DR WPI; 2001-032104/04.		CC (APP) Abeta fragments in the brain of a patient, which comprises
XX		CC (APP) Abeta fragments in the brain of a patient, which comprises
PT Preventing or treating a disease associated with amyloid deposits,		CC (APP) Abeta fragments in the brain of a patient, which comprises
PT especially Alzheimer's disease, comprises administering amyloid		CC antibody that binds to an amyloid deposit and induces a clearing response (FC
PT specific antibody		CC receptor mediated phagocytosis) against it (b) a polypeptide containing
XX		CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
PS Disclosure; Figure 19; 143pp; English.		CC that induces an immunogenic response against residues 1-3 to 7-11 of
XX		CC Abeta. The products of the invention have nootropic and neuroprotective
CC This invention describes a novel method of preventing or treating a		CC activity. The method is also useful for monitoring a course of treatment
CC disease associated with amyloid deposits of amyloid precursor protein		CC being administered to a patient e.g. active and passive immunization. The
CC (APP) Abeta fragments in the brain of a patient, which comprises		CC methods are useful for prophylactic and therapeutic treatment of
CC administering to the patient: (a) an antibody that binds to Abeta, the		CC Alzheimer's disease.
CC antibody binds to an amyloid deposit and induces a clearing response (FC		XX SQ Sequence 10 AA;
CC receptor mediated phagocytosis) against it (b) a polypeptide containing		XX Query Match 80.0%; Score 8; DB 22; Length 10;
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent		XX Best Local Similarity 100.0%; Pred. No. 0.0066;
CC that induces an immunogenic response against residues 1-3 to 7-11 of		XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC Abeta. The products of the invention have nootropic and neuroprotective		Qy 1 AEFRHDSG 8
CC activity. The method is also useful for monitoring a course of treatment		Db 3 AEFRHDSG 10
CC being administered to a patient e.g. active and passive immunization. The		
CC methods are useful for prophylactic and therapeutic treatment of		
XX		RESULT 6
SQ Sequence 10 AA;		AAB46216
Query Match 90.0%; Score 9; DB 22; Length 10;		ID AAB46216 standard; peptide; 10 AA.
Best Local Similarity 100.0%; Pred. No. 0.0049;		XX
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		AC AAB46216;
Qy 2 EFRHDSGY 10		XX DT 04-APR-2001 (first entry)
Db 1 EFRHDSGY 9		XX DE Human APP derived immunogenic peptide #12.
RESULT 5		XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
AAB46212		KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;
ID AAB46212 standard; peptide; 10 AA.		KW amyloid precursor protein; Alzheimer's disease.
XX		XX OS Homo sapiens.
AC AAB46212;		XX PN WO200072880-A2.
XX		XX

XX Modulating activity of beta-site amyloid precursor protein-cleaving
 XX PT enzyme secretase/sheddase for treatment of neurodegenerative disorder
 XX PT characterised by generation of Abeta protein, by preventing cleavage of
 XX PT enzyme
 XX PS Disclosure; Page 28; 64pp; English.
 XX
 CC This invention relates to a novel method for modulating activity of
 CC beta-site amyloid precursor protein (APP)-cleaving enzyme (BACE)
 CC secretase/sheddase. Cleavage of BACE by this enzyme results in the
 CC generation of a soluble BACE which enhances the production of the
 CC amyloidogenic Peptide Abeta which has been shown to be involved in the
 CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
 CC achieved by administration of an antisense nucleotide molecule capable
 CC of hybridising with BACE mRNA, by using a ribozyme that targets and
 CC degrades BACE secretase mRNA, with a peptide that can interfere with
 CC binding of the enzyme with BACE or using an antibody or antagonist that
 CC can function as an inhibitor of BACE secretase activation. The methods
 CC of the invention modulate the activity of BACE secretase/sheddase by
 CC preventing cleavage of BACE, which is useful for the treatment of a
 CC neurodegenerative disorder characterised by the generation of Abeta
 CC peptide, especially Alzheimer's disease. The invention also comprises a
 CC method for identification of an agent that can alter the ability of BACE
 CC secretase to associate with and process a known substrate, thus method
 CC can be used for high throughput screening of candidate molecules. The
 CC invention also comprises a method for determining whether an individual
 CC is at risk of developing a neurodegenerative disorder characterised
 CC by the generation of Abeta protein by measuring the levels of BACE
 CC C terminal cleavage products in a sample or tissue where an increase
 CC in cleavage products indicates a person at risk. The present sequence
 CC represents the N terminal of a beta amyloid protein of the
 CC invention.
 XX Sequence 8 AA;
 SQ Query Match 70.0%; Score 7; DB 23; Length 8;
 SQ Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 SQ Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ YY 1 AEFRHDS 7
 SQ Db 2 AEFRHDS 8
 RESULT 8
 AU78518 standard; Peptide; 8 AA.
 X AAB46211 standard; peptide; 10 AA.
 X AC AAB46211;
 X XX AAB46211;
 X DT 04-APR-2001 (first entry)
 X DE Human APP derived immunogenic peptide #7.
 X XX Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 X KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 X KW amyloid precursor protein; Alzheimer's disease.
 X XX Homo sapiens.
 X OS WO200210354-A2.
 X XX WO200072880-A2.
 X PN XX
 X PD XX
 X 07-FEB-2002. 07-DEC-2000.
 X X 01-AUG-2001; 2001WO-CA01118. 26-MAY-2000; 2000WO-US14810.
 X X 01-AUG-2000; 2000CA-2311828. 28-MAY-1999; 99US-0322289.
 X X (RECL) INST RECH CLINIQUES MONTREAL. XX (NEUR-) NEURALAB LTD.
 X X Seidah NG, Chretien M, Cromlish JA; Schenk DB, Bard F, Vasquez NJ, Yednock T;
 X X WPTI: 2002-280612/32.

DR WPI; 2001-032104/04.
 XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX Disclosure; Figure 19; 143pp; English.

PS XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-5 of Abeta; or (c) an agent
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

XX SQ Sequence 10 AA;

Query Match 70.0%; Score 7; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFRHDS 7
 Db 4 AEFRHDS 1.0

RESULT 9
 AAB46217 ID AAB46217 standard; peptide; 10 AA.
 XX AC AAB46217;
 XX DT 04 - APR - 2001 (first entry)
 XX DE Human APP derived immunogenic peptide #13.
 XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO200072880-A2.
 XX PD 07 - DEC - 2000.
 XX PR 26 - MAY - 2000; 2000WO-US14810.
 XX PS 28 - MAY - 1999; 99US - 0322289.
 XX PA (NEUR-) NEURALAB LTD.

XX PD 07 - DEC - 2000.
 XX PI Schenck DB, Bard F, Vasquez NJ, Yednock T;
 XX PF 26 - MAY - 2000; 2000WO-US14810.
 XX DR 2001-032104/04.
 XX PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

XX SQ Sequence 7 AA;

DR WPI; 2001-032104/04.
 XX antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

XX SQ Sequence 10 AA;

Query Match 70.0%; Score 7; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RHDSGYE 10
 Db 1 RHDSGYE 7

RESULT 10
 AAB46202 ID AAB46202 standard; peptide; 7 AA.
 XX AC AAB46202;
 XX DT 04 - APR - 2001 (first entry)
 XX DE Human APP A-beta protein N-terminal fragment.
 XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO200072880-A2.
 XX PD 07 - DEC - 2000.
 XX PR 26 - MAY - 2000; 2000WO-US14810.
 XX PS 28 - MAY - 1999; 99US - 0322289.
 XX PA (NEUR-) NEURALAB LTD.
 XX PI Schenck DB, Bard F, Vasquez NJ, Yednock T;
 XX DR 2001-032104/04.
 XX PD 07 - DEC - 2000.
 XX PR 26 - MAY - 1999; 99US - 0322289.
 XX PA (NEUR-) NEURALAB LTD.

XX PD 07 - DEC - 2000.
 XX PI Schenck DB, Bard F, Vasquez NJ, Yednock T;
 XX PF 26 - MAY - 2000; 2000WO-US14810.
 XX DR 2001-032104/04.
 XX PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

XX SQ Sequence 7 AA;

RESULT 1.3
 AAB46210 standard; peptide: 10 AA.
 ID XX
 AC AAB46210;
 DT 04-APR-2001 (first entry)
 XX DE Human APP derived immunogenic peptide #6.
 XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO200072880-A2.
 PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US14810.
 XX PR 28-MAY-1999; 99US-0322289.
 PA (NEUR-) NEURALAB LTD.
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 DR WPI; 2001-032104/04.
 PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 PS Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (FC
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 SQ Sequence 10 AA;
 Query Match Score 6; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PS Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (FC
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 SQ Sequence 10 AA;
 Query Match Score 6; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1.4
 AAB46218 standard; peptide: 10 AA.
 ID XX
 AC AAB46218;
 DT 04-APR-2001 (first entry)
 XX DE Human APP derived immunogenic peptide #14.
 XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;

KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO200072880-A2.
 PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US14810.
 XX PR 28-MAY-1999; 99US-0322289.
 PA (NEUR-) NEURALAB LTD.
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 DR WPI; 2001-032104/04.
 PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 PS Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (FC
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 SQ Sequence 10 AA;
 Query Match Score 6; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PS Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (FC
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 SQ Sequence 10 AA;
 Query Match Score 6; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PS Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (FC
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 SQ Sequence 10 AA;
 Query Match Score 6; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PS Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (FC
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

RESULT 1.5
 ABB05182 standard; peptide: 5 AA.
 ID XX
 AC ABB05182;
 DT 02-APR-2002 (first entry)
 DE Beta amyloid peptide related peptide PPI-339 SEQ ID NO:36.
 XX KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;
 KW APP-770; amyloid aggregation; Alzheimer's disease;
 KW nootropic; neuroprotective; immunosuppressive; antimicrobial; auditory;
 KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotoxic;
 KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
 KW amyloidogenic disease; beta amyloid deposition; amyloidosis;
 KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
 XX OS Homo sapiens.
 XX Synthetic.
 PN US6319498-B1.
 XX

PD 20-NOV-2001.
 XX
 PF 14-MAR-1986; 96US-0617267.
 XX
 PR 14-MAR-1995; 95US-0404831.
 PR 07-JUN-1995; 95US-0475579.
 PR 27-OCT-1995; 95US-0548998.
 XX
 PA (PRAE-) PRAEACTS PHARM INC.
 XX
 PI Findels MA, Benjamin H, Garnick MB, Gefter ML, Hundal A, Kasman L;
 PI Musso G, Signer ER, Wakefield J, Reed MJ;
 XX DR WPI; 2002-146668/19.

XX Amyloid modulator compound useful for treatment of an amyloidogenic disease such as Alzheimer's disease comprises an aggregation core domain and a modifying group attached to it

XX PS Example 11; Column 63; 54pp; English.

CC The present invention describes an amyloid modulator compound (I) comprising an aggregation core domain and a modifying group attached to it. (I) has nocropic, neuroprotective, immunosuppressive, antimicrobial, antidiabetic, antipyretic, dermatological, cardiological, nephrotoxic and auditory activities, and can be used as a natural amyloid aggregation inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide (beta-AP). (I) are used in the manufacture of a medicament for the diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's disease and other clinical occurrences of beta amyloid deposition such as Down's syndrome individuals and in patients with hereditary cerebral haemorrhage with amyloidosis, and for treating a disorder associated with amyloidosis such as familial amyloid polyneuropathy. (I) reduces the toxicity of natural beta-AP aggregates to cultured neuronal cells. (I) not only reduces the formation of neurotoxic aggregates but also have the ability to reduce the neurotoxicity of performed A-beta fibrils. The present sequence represents a peptide which is used in the exemplification of the present invention.

XX Sequence 5 AA;

Query Match 50.0%; Score 5; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 HDSGY 9
 Db 1 HDSGY 5

Search completed: April 21, 2003, 12:40:44
 Job time : 29.5 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:38:43 ; Search time 23.5 Seconds
 (without alignments)
 87.680 Million cell updates/sec

Title: US-09-580-018-6
 Perfect score: 10
 Sequence: VKMDFRHD 10

Scoring table: OLIGO

Gapext 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1223

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : SPREMBL_21;*

1: sp_archea;*

2: sp_bacteria;*

3: sp_fungi;*

4: sp_human;*

5: sp_invertebrate;*

6: sp_mammal;*

7: sp_mhc;*

8: sp_organelle;*

9: sp_phage;*

10: sp_plant;*

11: sp_rabbit;*

12: sp_virus;*

13: sp_vertebrate;*

14: sp_unclassified;*

15: sp_rvirus;*

16: sp_bacteriap;*

17: sp_archaeap;*

Score	Match	Length	DB	ID	Description
17	2	20.0	20.0	Q9r3X0	planktothri
18	2	20.0	20.0	Q9rL7	ciostridium
19	2	20.0	20.0	Q0503	saccharomy
20	2	20.0	20.0	Q9urb9	saccharomy
21	2	20.0	20.0	Q15901	homo sapien
22	2	20.0	20.0	Q9YJ4	homo sapien
23	2	20.0	20.0	Q60773	homo sapien
24	2	20.0	20.0	Q9UB13	albinaria h
25	2	20.0	20.0	P82686	periplaneta
26	2	20.0	20.0	Q9gmh3	lagenorhynch
27	2	20.0	20.0	Q28866	megaptera n
28	2	20.0	20.0	Q8WNS1	bos taurus
29	2	20.0	20.0	Q9TRX8	bos taurus
30	2	20.0	20.0	Q9RFC3	didelphis m
31	2	20.0	20.0	Q9BFC2	macropus eu
32	2	20.0	20.0	Q9BFC1	choloepus h
33	2	20.0	20.0	Q9BFC0	choloepus d
34	2	20.0	20.0	Q9BFB9	euphractus d
35	2	20.0	20.0	Q9BFB8	chaetophrac
36	2	20.0	20.0	Q9BFB7	tamandua te
37	2	20.0	20.0	Q9BFB6	myrmecophag
38	2	20.0	20.0	Q9BFB5	erinaceus c
39	2	20.0	20.0	Q9BFB4	talpa altai
40	2	20.0	20.0	Q9BFB3	condylura c
41	2	20.0	20.0	Q9BFB2	soxex arane
42	2	20.0	20.0	Q9FBF1	echinops te
43	2	20.0	20.0	Q9FBF0	trichechus
44	2	20.0	20.0	Q9BFA9	procavia ca
45	2	20.0	20.0	Q9BFA8	loxodont a

ALIGNMENTS

Result	1	
ID	P72149	PRELIMINARY;
AC	P72149;	PRT;
DT	01-FEB-1997 (TREMBLref. 02; Created)	9 AA.
DT	01-FEB-1997 (TREMBLref. 02; Last sequence update)	
DT	01-DEC-2001 (TREMBLref. 19; Last annotation update)	
DE	Putative glucokinase (Fragment).	
GN	GLK.	
OS	Pseudomonas aeruginosa.	
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	
OX	Pseudomonas.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=PAO1;	
RX	MEDLINE=9627344; PubMed=8830708;	
RA	Sage A.E., Proctor W.D., Phibbs P.V.J.R.;	
RT	A two-component response regulator, glnR, is required for glucose transport activity in Pseudomonas aeruginosa PAO1.";	
RL	J. Bacteriol. 178:6064-6066(1996).	
DR	U50932; AAC44474.1; -.	
KW	Kinase.	
FT	NON_TER	
SQ	SEQUENCE	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	3	30.0	9	2	P72149	P72149 pseudomonas	P72149 MW C3071DDAA72DC6C6 CRC64;
2	3	30.0	10	12	Q9j1g8	Q9j1g8 tt virus. o	Q9j1g8 tt virus. o
3	2	20.0	7	2	Q47477	Q47477 escherichia	Q47477 escherichia
4	2	20.0	7	4	Q15897	Q15897 homo sapien	Q15897 homo sapien
5	2	20.0	7	6	Q28742	Q28742 oryctolagus	Q28742 oryctolagus
6	2	20.0	7	8	Q98666	Q98666 spinacia ol	Q98666 spinacia ol
7	2	20.0	7	11	Q55184	Q55184 ratius norv	Q55184 ratius norv
8	2	20.0	7	12	Q9YVE3	Q9YVE3 human adeno	Q9YVE3 human adeno
9	2	20.0	7	12	Q9YTR0	Q9YTR0 human adeno	Q9YTR0 human adeno
10	2	20.0	7	12	Q9TI09	Q9TI09 human adeno	Q9TI09 human adeno
11	2	20.0	8	2	Q68485	Q68485 klebsiella	Q68485 klebsiella
12	2	20.0	8	2	Q9SESD5	Q9SESD5 escherichia	Q9SESD5 escherichia
13	2	20.0	8	2	P72221	P72221 pseudomonas	P72221 pseudomonas
14	2	20.0	8	2	Q9RTT2	Q9RTT2 escherichia	Q9RTT2 escherichia
15	2	20.0	8	2	P83158	P83158 anaerena sp	P83158 anaerena sp
16	2	20.0	8	2	P83152	P83152 anaerena sp	P83152 anaerena sp

Result	2	
ID	Q9J1G8	PRELIMINARY;
AC	Q9J1G8;	PRT;
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=PAO1;	
RX	MEDLINE=9627344; PubMed=8830708;	
RA	Sage A.E., Proctor W.D., Phibbs P.V.J.R.;	
RT	A two-component response regulator, glnR, is required for glucose transport activity in Pseudomonas aeruginosa PAO1.";	
RL	J. Bacteriol. 178:6064-6066(1996).	
DR	U50932; AAC44474.1; -.	
KW	Kinase.	
FT	NON_TER	
SQ	SEQUENCE	

Query Match 30.0%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DAE 6
 |||
 Db 6 DAE 8

DT	01-OCT-2000 (TREMBLrel. 15, Created)	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	OX	NCBI_TaxID=9606;		
DE	ORF2.	RN	[1]		
OS	"virus.	RP	SEQUENCE FROM N.A.		
FT	virus;	RC	TISSUE=PLACENTA;		
SQ	ssDNA viruses; unclassified ssDNA viruses.	RA	Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,		
NCBI_TaxID=68887;		RA	Coolbaugh M.I., Chinault C.A., Bairdini A., Lindsay E.A., Zhao Z.-Y.,		
[1]	RN	RA	Caskey C.T.H.,		
RP	SEQUENCE FROM N.A.	RA	RT Isolation of chromosome-specific genes by reciprocal probing of		
RC	STRAIN=PTV-SC232;	RT	arrayed cDNAs and cosmid libraries.,";		
RX	MEDLINE=20251008; PubMed=10790123;	RL	Human Mol. Genet. 0:0 (1995).		
RA	Nie J.C., Saback F.L., Lampe E.;	DR	EMBL: L32077; AAA73887.1; -.		
RT	"Coinfection with Multiple TT Virus Strains Belonging to Different	FT	NON_TER 1 1		
RT	Genotypes Is a Common Event in Brazilian Healthy Adults.";	FT	NON_TER 7 7		
J. CLIN. MICROBOL.	38:1926-1930(2000).	SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;	Query Match 20.0%; Score 2; DB 4; Length 7;		
DR	EMBL: AF216455; AAFF66889; 1; -.	Best Local Similarity 100.0%; Pred. No. 6.7e+05;	Best Local Similarity 100.0%; Pred. No. 6.7e+05;		
SEQUENCE	-10 AA; 1124 MW;	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
SQ	64FF2BD771B5B9CB CRC64;	Qy 5 AE 6	Qy 5 AE 6		
Qy	5 AEF 7	Db 5 AE 6	Db 5 AE 6		
Db	1 1				
Db	2 AEF 4				
RESULT 3	Q47477	PRELIMINARY; PRT; 7 AA.	RESULT 5	Q28742	PRELIMINARY; PRT; 7 AA.
ID	Q47477	PRELIMINARY; PRT; 7 AA.	ID	Q28742	PRELIMINARY; PRT; 7 AA.
AC	Q47477;	PRT; 7 AA.	AC	Q28742;	PRELIMINARY; PRT; 7 AA.
DT	01-NOV-1996 (TREMBLrel. 01, Created)	DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)	DE	Alpha-myosin heavy chain (Fragment).		
DE	TPI protein (Fragment).	OS	Oryctolagus cuniculus (Rabbit).		
GN	TPI.	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OS	Escherichia coli.	OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagrus.		
OC	Escherichia.	OX	NCBI_TaxID=9986;		
OC	Escherichia.	RN	[1]		
OX	NCBI_TaxID=562;	RP	SEQUENCE FROM N.A.		
RN	[1]	RX	MEDLINE=84221901; PubMed=6328491;		
RP	SEQUENCE OF 7-7 FROM N.A.	RA	Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovicic S.,		
AC	01-JUL-1997; PubMed=3158524;	RA	Rabinowitz M.;		
RX	MEDLINE=82203917; PubMed=3158524;	RT	"Characterization of genomic clones specifying rabbit alpha- and beta-		
RA	Helling H.W., Evans P.R.;	RT	ventricular myosin heavy chains.,";		
RT	"Nucleotide sequence and high-level expression of the major	RL	Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).		
RT	Escherichia coli phosphotriokinase."	DR	EMBL: K01698; AAA31415.1; -.		
ER	Eur. J. Biochem. 149:363-373(1985).	FT	NON_TER 1 1		
RN	[2]	SQ	SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;		
RP	SEQUENCE FROM N.A.	Query Match 20.0%; Score 2; DB 6; Length 7;			
RA	Evans P.	Best Local Similarity 100.0%; Pred. No. 6.7e+05;			
RA	Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
RL	DR	Qy 2 KM 3			
DR	X02519; CRA26359.1; -.	Db 2 KM 3			
FT	NON_TER 1 1				
SEQUENCE	7 AA; 773 MW;	Qy 5 AE 6			
SQ	7416D33DDDB1DB0 CRC64;	Db 1 AE 2			
Query Match 20.0%; Score 2; DB 2; Length 7;					
Best Local Similarity 100.0%; Pred. No. 6.7e+05;					
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
RESULT 4	Q15897	PRELIMINARY; PRT; 7 AA.	RESULT 6	Q98866	PRELIMINARY; PRT; 7 AA.
ID	Q15897;	PRT; 7 AA.	ID	Q98866	PRELIMINARY; PRT; 7 AA.
AC	Q15897;	PRT; 7 AA.	AC	Q98866;	PRELIMINARY; PRT; 7 AA.
DT	01-NOV-1996 (TREMBLrel. 01, Created)	DT	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DE	Cytochrome b/f subunit IV (Fragment).		
DE	(clone XP6A11A) (Fragment).	OS	Spinacia olaracea (Spinach).		
DE	Homo sapiens (Human).	OG	Chloroplast.		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Spermatophyta; Magnoliophyta; Caryophyllales; Chenopodiaceae; Spinacia.	OC	Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.		
OX	NCBI_TaxID=35562;	OX	NCBI_TaxID=9606;		

RN [1] SEQUENCE FROM N.A.
RP MEDLINE=86120353; PubMed=3003688;
RX Sjöben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RA "Spinach plastid genes coding for initiation factor IF-1, ribosomal
protein S11 and RNA polymerase alpha-subunit.";
RT Protein S11 and RNA Polymerase alpha-subunit.;
RL Nucleic Acids Res. 14:1029-1044(1986).
DR EMBL: X03426; CAA27215.1;
KW Chloroplast.

FT NON-TER 1 AA; 907 1 MW; 644729D77409c420 CRC64;

SEQUENCE 7 AA; 907 1
Best Local Similarity 20.0%; Score 2; DB 8; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FR 8
Db 1
2 FR 3

RESULT 7
ID 055184 PRELIMINARY; PRT; 7 AA.
AC 055184;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Orphan receptor TR4 NS (Fragment).
GN TR4.
OS Rat.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96129976; PubMed=8612486;
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D., Chuang D.M.,
RA Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
of novel sequences in the 5'-untranslated region and C-terminal
domain.";
RT Endocrinology 137:1562-1571(1996).
RN [2] SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=96129976; PubMed=8661150;
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
expression and chromosomal localization of the human gene.";
RL Genomics 35:361-366(1996).
DR EMBL: U59454; AAB91433.1; -.
KW Receptor.
FT NON-TER 1 AA; 663 MW; 6DDAA8787EB05350 CRC64;

SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 20.0%; Score 2; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DA 5
Db 6 DA 7

RESULT 8
Q9YVE3 PRELIMINARY; PRT; 7 AA.
ID Q9YVE3
AC 09YVE3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

SEQUENCE FROM N.A.
RC STRAIN=GOMEI;
RX MEDLINE=99173282; PubMed=10074533;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute
respiratory disease.";
RL J. Clin. Microbiol. 37:1107-1112(1999).
RN [2] SEQUENCE FROM N.A.
RC STRAIN=GOMEI;
RA Crawford-Miksza L.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF065065; AAD03662.1; -.
FT NON-TER 1 AA; 980 MW; 7B5EA414140322A0 CRC64;

SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 20.0%; Score 2; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VK 2
Db 1 VK 2

RESULT 9
Q9YVRO PRELIMINARY; PRT; 7 AA.
ID Q9YVRO
AC Q9YVRO; 10' Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PVI core protein (Fragment).
GN PVI.
OS Human adenovirus type 7a.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae, Mastadenovirus.
OX NCBI_TaxID=85755;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.T96-0620, S-1058, AND CL 68578;
RC Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF065066; AAD03664.1; -.
DR EMBL; AF065067; AAD03666.1; -.
FT NON-TER 1 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 20.0%; Score 2; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VK 2
Db 1 VK 2

RESULT 10
Q9YVQ9 PRELIMINARY; PRT; 7 AA.
ID Q9YVQ9
AC Q9YVQ9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE PVI core protein (Fragment).

PVI.	OX NCBI_TAXID=562;
OS Human adenovirus type 4.	RN [1]
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.	RP SEQUENCE FROM N.A.
OX NCBI_TAXID=28280;	RC STRAIN=A295B;
RN RP SEQUENCE FROM N.A.	RX MEDLINE-99194747; PubMed=10094716;
SEQUENCE FROM N.A. STRAIN=Z_G_95-873, RI-67, AND 55142;	RA Rahn A., Drummond Smith J., Whitfield C.;
Crawford Mikenza L.K., Nang R.N., Schuhur D.P.;	RT "Conserved organization in the cps gene clusters for expression of
"Molecular surveillance of strain variation in adenoviruses causing	RT Escherichia coli group 1 K antigens: relationship to the colanic acid
acute respiratory disease, AV 4 and AV 7a.";	RT biosynthesis locus and the cps genes from Klebsiella pneumoniae.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.	RL J. Bacteriol. 181:2307-2313(1999).
EMBL; AF065064; ADD3659.1; -.	DR EMBL; AF118251; ADD30008.1; -.
EMBL; AF065064; ADD3653.1; -.	FT NON_TER 8
EMBL; AF065063; ADD3656.1; -.	SQ SEQUENCE 8 AA; 1011 MW; F21DC1A9D1B41406 CRC64;
NON_TER 1	Query Match 20.0%; Score 2; DB 2; Length 8;
SEQUENCE 7 AA; 980 MW;	Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VK 2	RESULT 13
Db 1 VK 2	P72221 PRELIMINARY; PRT; 8 AA.
Db 1 VK 2	ID P72221; PRELIMINARY; PRT; 8 AA.
RESULT 11	AC P72221; PRELIMINARY; PRT; 8 AA.
068485	PRELIMINARY; PRT; 8 AA.
ID 068485	AC P72221; PRELIMINARY; PRT; 8 AA.
068485;	DT 01-FEB-1997 (TREMBLrel. 02, Created)
068485;	DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
01-AUG-1998 (TREMBLrel. 07, Created)	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
01-AUG-1998 (TREMBLrel. 07, Last sequence update)	DE Alginicante lyase (fragment).
01-MAR-2002 (TREMBLrel. 20, Last annotation update)	GN ALY.
Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).	OS Pseudomonas sp. (strain OS-ALG-9).
AADAL.	OC Bacteria; Proteobacteria.
Klebsiella pneumoniae.	OX NCBI_TAXID=86338;
Plasmid pQ1000.	RN [1]
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	RP SEQUENCE FROM N.A.
Klebsiella.	RC STRAIN=OS-ALG-9;
NCBI_TAXID=573;	RA Fujiyama K.;
OX	RL Submitted (Oct-1994) to the EMBL/GenBank/DDBJ databases.
NCBI_TAXID=573;	RN [2]
RN SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.KL;	RC STRAIN=OS-ALG-9;
RX MEDLINE-98287600; PubMed=8336113;	RX MEDLINE-93323366; PubMed=8336113;
RA Centro D., Roy P.H.;	RA Makii H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene	RT Cloning, sequence analysis and expression in Escherichia coli of a
aac(6')-Ig from the integron of a natural multiresistance plasmid.";	RT gene encoding an alginicate lyase from Pseudomonas sp. OS-ALG-9.";
Antimicrob. Agents Chemother. 42:1506-1508(1998).	RL J. Gen. Microbiol. 139:987-993(1993).
EMBL; AF07556; AAC25501.1; -.	DR EMBL; D38469; BAA21704.1; -.
Plasmid; Transferase.	KW Lyase.
NON_TER 8	FT NON_TER 1 1
SEQUENCE 8 AA; 878 MW;	SQ SEQUENCE 8 AA; 841 MW; 461DDDC5A5B041BB CRC64;
FT	Query Match 20.0%; Score 2; DB 2; Length 8;
SEQUENCE 8 AA;	Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 AE 6	RESULT 14
Db 3 AE 4	Q9RRT2 PRELIMINARY; PRT; 8 AA.
Db 7 AE 8	AC Q9RRT2; PRELIMINARY; PRT; 8 AA.
RESULT 12	AC Q9RRT2; PRELIMINARY; PRT; 8 AA.
Q9S6D5	PRELIMINARY; PRT; 8 AA.
ID Q9S6D5	AC Q9RRT2; PRELIMINARY; PRT; 8 AA.
Q9S6D5;	DT 01-MAY-2000 (TREMBLrel. 13, Created)
01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
01-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
Putative IS30 transposase (Fragment).	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Escherichia coli.	DE Hypothetical 1.0 kDa protein (Fragment).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae.	GN YQFG.
Escherichia.	OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N12;

RX MEDLINE=97061202; PubMed=8905232;
 RA Ohshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikehito K.,
 RA Ikehito K., Inada T., Itoh T., Katahara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
 RA Sampai G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiechi T.;
 RT "A 7.18-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
 RT to the 12.7-28.0 min Region on the Linkage Map.";
 RL DNA Res. 3:137-155(1996);
 DR EMBL; D90705; BAA3510; -.

KW Hypothetical protein.

FT NON_TER 1

SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AE 6
 |
 Db 5 AE 6

RESULT 15

P83158 PRELIMINARY; PRIT; 8 AA.
 ID P83158
 AC P83158;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE Photosystem I iron-sulfur center (Photosystem I subunit VII) (9 kDa
 polypeptide) (PSI-C) (Fragment).
 OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=29412;

RN SEQUENCE.
 RA Apté S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.

CC -!- FUNCTION: APOROTEPIN FOR THE IRON-SULFUR CENTERS FA AND FB OF THE
 PHOTOSYSTEM I COMPLEX.

CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
 CC 'AERIAL-TYPE' 4Fe-4S FERREDOXINS.

DR INTPRO; IPRED0450; 4Fe4S_FERREDOXIN.

DR PROSITE; PS00198; 4FE4S_FERREDOXIN; PARTIAL.

KW Photosynthesis; Photosystem I; Iron-sulfur; 4Fe-4S; Metal-binding.

FT NON_TER 8

SQ SEQUENCE 8 AA; 962 MW; C5BB505322D1A1F5 CRC64;

Query Match 20.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VK 2
 |
 Db 4 VK 5



Result No.	Score	Query ID	Match	Length	DB ID	Description
1	2	20.0	5	1	RE21_LITRU	P82071 litoria rub
2	2	20.0	5	1	RE3_LITRU	P82072 litoria rub
3	2	20.0	6	1	FARP_MONEX	P41966 moniezia ex
4	2	20.0	6	1	TRPL_PSEPU	P36414 pseudomonas
5	2	20.0	6	1	UN06_CLOPA	P81351 clostridium
6	2	20.0	7	1	ALI7_CYDPO	P82158 cydia pomon
7	2	20.0	7	1	FARI_ASCSU	P31889 ascaris suu
8	2	20.0	7	1	UF03_MOUSE	P38641 mus musculus
9	2	20.0	8	1	CCRN_MACBEU	P30369 macropus eu
10	2	20.0	8	1	GJUR_HUMAN	P02729 homo sapien
11	2	20.0	8	1	LCK4_LEDIMA	P2143 leucophaea
12	2	20.0	8	1	PPK3_PERFAM	P82455 orconectes
13	2	20.0	8	1	UC26_MAIZE	P82618 periplaneta
14	2	20.0	8	1	CXOE_THROB	P80632 zea mays (m
15	2	20.0	9	1	DSTP_RABTT	P01158 orctocotyle
16	2	20.0	9	1	FTIB_PAPAN	P19344 papilio anubis
17	2	20.0	9	1	IPTR_RHOVI	P82992 rhodopsebudo
18	2	20.0	9	1	NEUT_CAVPO	P34966 cavia porce
19	2	20.0	9	1	NEUX_HUMAN	P04277 homo sapien
20	2	20.0	9	1	OXTT_OCTIVU	P80027 octopus vulgaris
21	2	20.0	9	1	ULAD_HUMAN	P31929 homo sapien
22	2	20.0	9	1	XYLA_SPSRQ	P19149 streptomyces
23	2	20.0	9	1	CABR_LITXA	P56264 litoria xanthina
24	2	20.0	10	1	COTO_THUOB	P80982 thunnus obesus
25	2	20.0	10	1	FARP_MYTED	P42560 mytilus edulis
26	2	20.0	10	1	FIIB_CERSI	P14537 ceratotherium
27	2	20.0	10	1	GLEM_HUMAN	P02728 homo sapiens
28	2	20.0	10	1	GON3_PETMA	P30948 petromyzon
29	2	20.0	10	1	MALE_KLEPN	Q05564 klebsiella
30	2	20.0	10	1	PNEU_HUMAN	P22103 homo sapiens
31	2	20.0	10	1	PNEU_RAT	P21996 ratmus norvegicus
32	2	20.0	10	1	Q2OG_COMTEA	P80466 comamonas t

ALIGNMENTS						
RESULT 1						
ID	RE21_LITRU	STANDARD;	PRT;	5 AA.		
AC	P82071;					
DT	15-JUN-2002 (Rel. 41, Created)					
DT	15-JUN-2002 (Rel. 41, Last sequence update)					
DT	15-JUN-2002 (Rel. 41, Last annotation update)					
DE	Rubellidin 2.1.					
OS	Litoria rubella (Desert tree frog).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Pelodytidae; Litoridae.					
OX	NCBI_TAXID=104895;					
RN	SEQUENCE, AND MASS SPECTROMETRY.					
RC	TISSUE=Skin secretion;					
RA	Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;					
RT	"The structure of new peptides from the Australian red tree frog Litoria rubella. the skin peptide profile as a probe for the study of evolutionary trends of amphibians."					
RT	Aust. J. Chem. 49:955-953(1996).					
RL	-1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBOTIC ACTIVITY.					
CC	CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.					
CC	CC -!- MASS SPECTROMETRY: MW=628; METHOD=FAB.					
KW	Amphibian skin.					
SQ	SEQUENCE 5 AA: 626 MW: 6DD9C9CB10300000 CRC64;					
Query Match	20.0%	Score 2;	DB 1;	Length 5;		
Best Local Similarity	100.0%	Pred. No. 1.1e+05;				
Matches	2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	6 EF 7					
Db	1					
Db	2 EF 3					
RESULT 2						
ID	RE31_LITRU	STANDARD;	PRT;	5 AA.		
AC	P82072;					
DT	15-JUN-2002 (Rel. 41, Created)					
DT	15-JUN-2002 (Rel. 41, Last sequence update)					
DT	15-JUN-2002 (Rel. 41, Last annotation update)					
DE	Rubellidin 3.1.					
OS	Litoria rubella (Desert tree frog).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Pelodytidae; Litoridae.					
OX	NCBI_TAXID=104895;					
RN	SEQUENCE, AND MASS SPECTROMETRY.					
RC	TISSUE=Skin secretion;					
RA	Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;					

"The structure of new peptides from the Australian red tree frog 'Litoria rubella', the skin peptide profile as a probe for the study of evolutionary trends of amphibians.";
 Aust. J. Chem. 49:955-963 (1996).
 -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match	20.0%	Score 2;	DB 1;	Length 5;
Best Local Similarity	100.0%	Pred. No. 1..1e+05;		
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
Qy 6 EF 7				
Db 2 EF 3				

RESULT 3
 FARP_MONEX STANDARD; PRT; 6 AA.
 ID FARP_MONEX
 AC P41966;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE FMRFamide-like neuropeptide GNFRF-amide.
 OS Moniezia expansa (Sheep tapeworm).
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclopiliida; Anoplocephalida; Moniezia.
 OX NCBI_TaxID=26841;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=93312289; PubMed=8323531;
 RA Mauli A.G., Shaw C., Halton D.W., Thim L.;
 RT "GNRFamide: a novel FMRFamide-immunoreactive peptide isolated from the sheep tapeworm Moniezia expansa";
 RT Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
 -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 CC KW Neuropeptide; Amidation.
 FT MOD_RES 6 6 AMIDATION.
 SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match	20.0%	Score 2;	DB 1;	Length 6;
Best Local Similarity	100.0%	Pred. No. 1..1e+05;		
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
Qy 7 FR 8				
Db 4 FR 5				

RESULT 4
 TRP1_PSEPU STANDARD; PRT; 6 AA.
 ID TRP1_PSEPU
 AC P3614;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TRP1 operon transcriptional activator (Fragment).
 GN TRP1.
 OS Pseudomonas putida. Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.
 OC NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PG1 C1S;
 RX MEDLINE=8933526; PubMed=2503057;
 RA Eberly L.; Crawford I.P.;

DT	30-MAY-2000 (Rel. 39, Created)	AC P38641;
DT	30-MAY-2000 (Rel. 39, Last sequence update)	DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)	DT 01-OCT-1994 (Rel. 31, Last annotation update)
DE	Cydiastatin 7	DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
OS	Cydia pomonella (Codling moth).	OS Mus musculus (Mouse)
OC	Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;	OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OC	Diptera; Tortricoidea; Tortricidae; Olethreutinae; Cydia.	OX NCBI_TaxID=82600;
OX		OX NCBI_TaxID=10090;
RN	[1]	RN [1]
RP		RP SEQUENCE,
RC	SEQUENCE-Larva;	RC TISSUE=Epiblast;
RX	MEDLINE=98054539; PubMed=9392829;	RX MEDLINE=9500907; PubMed=7523108;
RA	Dave H., Johnsen A.H., Maistro J.-L., Scott A.G., Winstanley D.,	RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RA	Davey M., East P.D., Thorpe A.;	RT "Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
RT	"Lepidopteran peptides of the allatostatin superfamily.";	RL Electrophoresis 15:735-745(1994).
RL	Peptides 16:1301-1303(1991).	CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
CC	-!- SIMILARITY: BELONGS TO THE ALLOSTATIN FAMILY.	CC NON_TER 7
KW	Neuropeptide; Amidation.	SQ SEQUENCE 7 AA: 842 MW: 6AA7B1DDDB1B180 CRC64;
FT	MOD_RES 7 7 AMIDATION.	Query Match Score 2; DB 1; Length 7;
SEQUENCE	7 AA: 873 MW: 673879CABB569350 CRC64;	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Qy	2 KM 3	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 KM 2	QY 5 AE 6
Db	4 AE 5	DB 4 AE 5
<hr/>		
RESULT 7	FARI_ASCSU	RESULT 9
ID	FARI_ASCSU	CCKN_MACFU
AC	P31889;	STANDARD; PRT; 8 AA.
DT	01-JUL-1993 (Rel. 26, Created)	ID CCNK_MACFU
DT	01-JUL-1993 (Rel. 26, Last sequence update)	STANDARD; PRT; 8 AA.
DT	01-FEB-1996 (Rel. 33, Last annotation update)	AC P30369;
DE	FMRamide-like neuropeptide AFI.	DT 01-APR-1993 (Rel. 25, Created)
OS	Ascaris suum (pig roundworm) (Ascaris lumbricoides).	DT 01-APR-1993 (Rel. 25, Last sequence update)
OC	Eukaryota; Metazoa; Nematoidea; Chromadorea; Ascaridoidea;	DT 01-OCT-1996 (Rel. 34, Last annotation update)
OC	Ascarididae; Ascaris.	DE Cholecystokinin (CCK).
RN	[1]	GN CK.
RP		OS Macroptus eugenii (Tanner wallaby), and
RX	MEDLINE=9018045; PubMed=2622377;	OS Dasycurus viverrinus (Southeastern quoll).
RT	"AF1, a sequenced bioactive neuropeptide isolated from the nematode	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RT	Ascaris suum";	OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
RL	Neuron 2:1465-1473(1989)	OX NCBI_TaxID=9315, 9279;
CC	-!- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTORNEURONS. REDUCES THE INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE CELLS.	RN [1]
CC	-!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF GLANDIA PARTICULARLY IN THE ANTERIOR REGIONS.	RP SEQUENCE,
CC	-!- SIMILARITY: BELONGS TO THE FARP (FMRFamide RELATED PEPTIDE) FAMILY.	RC TISSUE=brain;
CC	Nervepeptide; Amidation.	RX MEDLINE=88234141; PubMed=3375140;
FT	MOD_RES 7 7 AMIDATION.	RT "Cholecystokinin octapeptide purified from brains of Australian marsupials".
SEQUENCE	7 AA: 953 MW: 69D4009CB144350 CRC64;	RT Fan Z.W., Eng J., Shaw G., Yallow R.S.;
SQ		RL Peptides 9:429-431(1988).
Qy	6 EF 7	CC -!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION AND THE RELEASE OF PANCREATIC ENZYMES IN THE GIT. ITS FUNCTION IN THE BRAIN IS NOT CLEAR.
Db	1 EF 4	CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
Db	3 EF 4	CC PIR: A43001; A43001.
Db	6 MD 7	DR PIR; PQ0012; PQ0012.
<hr/>		
RESULT 8	UF03_MOUSE	Query Match Score 2; DB 1; Length 8;
ID	UF03_MOUSE	Best Local Similarity 100.0%; Pred. No. 1.1e+05;
STANDARD;	PRT; 7 AA.	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	3 MD 4	QY 3 MD 4
Db	6 MD 7	DB 6 MD 7

	Db	1 DA 2
RESULT 10		
GLUR_HUMAN	STANDARD;	PRT; 8 AA.
ID P02729; HUMAN		
AC P02729; (Rel. 01, Created)		
DT 21-JUL-1986 (Rel. 01, Last sequence update)		
DT 21-JUL-1986 (Rel. 01, Last annotation update)		
DT 16-OCT-2001 (Rel. 40, Last sequence update)		
DE Urine glycopeptide.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Pancrustacea; Crustacea;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TaxID=9606;		
RN [1]		
RP SEQUENCE, MEDLINE=72062338; PubMed=5126885;		
RX RT Lote C.J.; Weiss J.B.;		
RA "Identification in urine of a low-molecular-weight highly polar		
RT glycopeptide containing cysteinyl-galactose."		
RL Biochem. J. 123:25P(1971).		
CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE		
IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN		
ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A		
SIMILAR STRUCTURE HAS ALSO BEEN FOUND.		
DR PIR: A03188; XGHUEU.		
KW GLycoprotein.		
FT CARBOHYD	1	S-LINKED (GAL-).
SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1E1 CRC4;		
Query Match Score 2; DB 1; Length 8;		
Best Local Similarity 100.0%; Pred. No. 1.1e+05;		
Patches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 9 HD 10		
Db 5 HD 6		
RESULT 11		
LCK4_LEUWA	STANDARD;	PRT; 8 AA.
ID LCK4_LEUWA		
AC P21113;		
DT 01-MAY-1991 (Rel. 18, Created)		
DT 01-MAY-1991 (Rel. 18, Last sequence update)		
DT 01-MAY-1991 (Rel. 18, Last annotation update)		
DB Leucophaea maderae (L-IV).		
OS Leucophaea maderae (Madeira cockroach).		
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;		
OC Blaberoidea; Blaberidae; Leucophaea.		
RN [1] LCK4_HEAD;		
RP SEQUENCE, AND SYNTHESIS.		
RA Holman G.M., Cook B.J., Nachman R.J.;		
RT "Primary structure and synthesis of two additional neuropeptides		
from Leucophaea maderae: members of a new family of		
Cephalomyotropins."		
RL Comp. Biochem. Physiol. 84C:271-276 (1986).		
CC -1- FUNCTION: THIS CEPAHOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE		
CC ACTIVITY OF COCKROACH PROTOPODUM (HINDGUT).		
CC -1- SIMILARITY: TO THE OTHER LEUCOKINTINS.		
KW FT MOD_RES 8 AMIDATION.		
SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;		
Query Match Score 2; DB 1; Length 8;		
Best Local Similarity 100.0%; Pred. No. 1.1e+05;		
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 4 DA 5		
RESULT 12		
ORMY_ORCLI	STANDARD;	PRT; 8 AA.
ID ORMY_ORCLI		
AC P82455;		
DT 16-OCT-2001 (Rel. 40, Created)		
DT 16-OCT-2001 (Rel. 40, Last sequence update)		
DT 16-OCT-2001 (Rel. 40, Last annotation update)		
DE Orconotropin (OMT).		
DE Orconectes limosus (Spinycheek crayfish).		
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;		
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;		
OC Astacida; Astacoidae; Cambaridae; Orconectes.		
OC NCBI_TaxID=28379;		
OX RN [1]		
RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.		
RC TISSUE-Hindgut;		
RX MEDLINE=20411310; PubMed=10952880;		
RA Dircksen H., Burdzik S., Sauter A., Keller R.;		
RT "Two orcokinins and the novel octapeptide orconotropin in the hindgut		
of the crayfish Orconectes limosus: identified myostimulatory		
neuropeptides originating together in neurones of the terminal		
RT abdominal ganglion."		
RL J. Exp. Biol. 203:2807-2818 (2000).		
CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND		
AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED		
BY ABDOMINAL GANGLIONIC NEURONS.		
CC -1- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.		
KW Amidation; Neuropeptide.		
FT MOD_RES 8 AMIDATION.		
SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDAA9 CRC64;		
Query Match Score 2; DB 1; Length 8;		
Best Local Similarity 100.0%; Pred. No. 1.1e+05;		
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 4 DA 5		
Db 2 DA 3		
RESULT 13		
PPK3_PPRAM	STANDARD;	PRT; 8 AA.
ID PPK3_PPRAM		
AC PR22618;		
DT 16-OCT-2001 (Rel. 40, Created)		
DT 16-OCT-2001 (Rel. 40, Last sequence update)		
DT 16-OCT-2001 (Rel. 40, Last annotation update)		
DE Pyrokinin-3 (Pea-PK-3) (FPXPL-amide).		
OS Periplaneta americana (American cockroach).		
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;		
OC Blattoidea; Blaberidae; Blattidae; Periplaneta.		
OX NCBI_TaxID=5978;		
RN [1]		
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.		
RC TISSUE-Retrocerebral complex;		
RX MEDLINE=9922469; PubMed=10196736;		
RA Prede R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;		
RT "Differential distribution of pyrokinin isoforms in cerebral and		
RT abdominal neurohemal organs of the American cockroach,"		
RL Insect Biochem. Mol. Biol. 29:139-144 (1999).		
RN [2]		
RP TISSUE SPECIFICITY		
RX MEDLINE=20169894; PubMed=10723010;		
RA Prede R., Eckert M.;		
RT "Praeger-specific distribution of FXPRlamides in the nervous system of		
the American cockroach,"		
RL J. Comp. Neurol. 419:352-363 (2000).		
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY		
CC (MYOTROPIC ACTIVITY).		
CC CC		

CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -1- MASS SPECTROMETRY: MW=906.5; METIOT=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT 8 AMIDATION.
 MOD_RES 8
 SEQUENCE 8 AA; 997 MW; 0B3A17409D772C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
 Best local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 FR 8
 Db 4 FR 5

RESULT 14
 UC26_MAIZE STANDARD; PRT; 8 AA..
 ID UC26_MAIZE
 AC P8032;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 NCBI_TaxID=4577;
 RN [1]
 RP
 RC
 TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 DR PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.
 CC Maize-2DPAGE; P80632; COLEOPTILE.
 FT 1
 NON_TER 1
 SQ. SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
 Best local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 AE 6
 Db 1 AE 2

RESULT 15
 COXE_THUOB STANDARD; PRT; 9 AA..
 ID COXE_THUOB
 AC P8075;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIA (EC 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 OC Elasmobranchii; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 NCBI_TaxID=8241;
 RN [1]
 RP
 RC TISSUE=heart;
 RX MEDLINE=9745291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,



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total number of hits

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Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : BIB 73 : *

pir1:*

3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by $\text{Pred. No.} = \frac{\text{No. of trials}}{\text{No. of trials}} \times \text{No. of trials}$.

A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Bysselein, V.E.; Ben Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intestine
A;Reference number: MUID:87153871; PMID:3826554
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SH2>
A;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystokinin-5
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide F
F;Modified site: amidated carboxyl end (Phe) #status experimental

RESULT 6
B31836 20K protein - Rickettsia rickettsii (fragment)
C;Species: Rickettsia rickettsii
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C;Accession: B31836
R;Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
A;Reference number: A91885; MUID:89008059; PMID:3139629
A;Accession: B31836
A;Molecule type: DNA
A;Residues: 1-5 <AND>
A;Cross references: GB:J03371; NID:9152455; PID:AAD15030.1; PID:94262874

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Qy	3 MD 4	20.0%	2	5	2	2;	100.0%	0	2.8e+05	0	0	0
Db	3 MD 4				1	MD 2						

RESULT 7
PQ0009 angiotsin-converting enzyme inhibitor (FLP-2) - common fig
N;Alternate names: ficus latex Peptide 2
C;Species: Ficus carica (common fig)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C;Accession: PQ0009
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica
A;Reference number: PQ0008
A;Accession: PQ0009
A;Molecule type: protein
A;Residues: 1-5 <MAR>
A;Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor

Query	Match	Score	DB	Length	Matches	Local	Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	3 MD 4	20.0%	2	5	2	2;	100.0%	0	2.8e+05	0	0	0
Db	3 MD 4				1	MD 2						

RESULT 4
C23751 spinal cord peptide SCP-6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C;Accession: C23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425; PMID:4015098
A;Accession: C23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <HST>
A;Superfamily: unassigned animal peptides

Query	Match	Score	DB	Length	Matches	Local	Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	4 DA 5	20.0%	2	5	2	2;	100.0%	0	2.8e+05	0	0	0
Db	4 DA 2				1	DA 2						

RESULT 5
B41225 copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: B41225
R;Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane
A;Reference number: A41225; MUID:92020961; PMID:1924351
A;Accession: B41225
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CHA>

Query	Match	Score	DB	Length	Matches	Local	Similarity	Pred.	No.	Mismatches	Indels	Gaps
Qy	5 AE 6	20.0%	2	5	2	2;	100.0%	0	2.8e+05	0	0	0
Db	5 AE 2				1	AE 2						

Db 1 AE 2

A; Residues: 1-5 <FEE>
A; Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
A; Accession: PT0539
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-5 <FEE>
A; Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H
A; Accession: PT0603
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-5 <FEE>
A; Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
C; Keywords: T-cell receptor

RESULT 9

A; Molecule type: Protein
A; Residues: 1-5 <CHT>
C; Species: Achatina fulica (giant African snail)
C; Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C; Accession: A44692
C; Status: translation not shown
R; Ohta, N.; Kubota, I.; Takao, T.; Shimomishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; NC
Biochem Biophys Res Commun. 178, 486-493, 1991
A; Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t
A; Reference number: A44692; MUID:91315471; PMID:1859408
A; Accession: A44692

A; Molecule type: Protein
A; Residues: 1-5 <CHT>
C; Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F; 2/Modified site: D-asparagine (Asn) #status experimental
F; 5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

S02617
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
C; Species: Equus caballus (domestic horse)
C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-1997
C; Accession: S02617
R; Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joernv
PEBS Lett. 222, 99-103, 1987
A; Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differ
A; Reference number: S02617; MUID:88005160; PMID:3653405
A; Accession: S02617
A; Molecule type: protein
A; Residues: 1-6 <FAU>
C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C; Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

S11024
hydroxensulfite reductase (EC 1.8.99.3) chain 1 - Desulfovibrio thermophilus (fragmen
N; Alternative names: bisulfite reductase; desulfofuscidin
C; Species: Desulfovibrio thermophilus
C; Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C; Accession: S11024
R; Faugue, G.; Lino, A.R.; Czechowski, M.; Kang, L.; Dervantarian, D.V.; Moura, J.J.G.
Biochim. Biophys. Acta 1040, 112-118, 1990
A; Title: Purification and characterization of bisulfite reductase (desulfofuscidin) f
A; Reference number: S11024; MUID:90335216; PMID:2165817
A; Accession: S11024
A; Molecule type: protein
A; Residues: 1-6 <FAU>
C; Keywords: oxidooreductase

Query Match Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

PT0538
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Accession: PT0538; PT0539; PT0603
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-5 <PEE>
A; Experimental source: newborn thymus, strain BALB/c, clone 100-2AE
A; Accession: PT0614
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-5 <PEE>
A; Experimental source: newborn thymus, strain BALB/c, clone 120-1H
C; Keywords: T-cell receptor

Query Match Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DA 5
Db 4 DA 5

RESULT 11

PT0538
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Accession: PT0538; PT0539; PT0603
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Status: translation not shown
A; Molecule type: mRNA

RESULT 14

A46474 Fc epsilon RIIB - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995

C;Accession: A46474

R;Richards, M.L.; Katz, D.H.; Liu, F.T.

J. Immunol. 147, 1067-1074, 1991

A;Title: Complete genomic sequence of the murine low affinity Fc receptor for IgE. Demon-

A;Reference number: A46474; PMID:1318149; PMID:1861070

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-6 <Ric>

A;Experimental source: BALB C, splenic B cells

A;Note: sequence extracted from NCBI backbone (NCBIP:45428)

Query Match 20.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MD 4

11

Db 1 MD 2

RESULT 15

PR0616 T-cell receptor beta chain V-D-J region (120-1G) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PR0616

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PR0509; PMID:91277601; PMID:1711558

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FEP>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DA 5

11

Db 4 DA 5

Search completed: April 21, 2003, 12:42:30

Job time :13 secs

GenCore version 5.1.4_ps-4578
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OM protein - protein search, using sw model1

Run on: April 21, 2003, 12:40:48 ; Search time 11.5 Seconds
(without alignments)
65.751 Million cell updates/sec

Title:	US-09-580-018-6
Perfect score:	10
-Sequence:	VKMDAEFRHD 10
Scoring table:	Oligo Gapext 60.0 , Gapext 60.0
Searched:	288829 seqs, 75613885 residues
Word size :	0
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Minimum DB seq length:	5
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Post-processing: Listing first 45 summaries

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	8	80.0	10	9	US-09-795-903A-4		Sequence 4, Appli
2	8	80.0	10	10	US-09-794-927-64		Sequence 64, Appli
3	8	80.0	10	10	US-09-795-847-64		Sequence 64, Appli
4	8	80.0	10	10	US-09-794-743-64		Sequence 64, Appli
5	8	80.0	10	10	US-09-794-748-54		Sequence 64, Appli
6	8	80.0	10	10	US-09-796-264-4		Sequence 64, Appli
7	8	80.0	10	10	US-09-794-925-64		Sequence 64, Appli
8	8	80.0	10	10	US-09-881-442-54		Sequence 64, Appli
9	8	80.0	10	10	US-09-845-226-14		Sequence 64, Appli
10	7	70.0	9	10	US-10-057-503-14		Sequence 10, Appli
11	7	70.0	7	10	US-09-867-047-5		Sequence 5, Appli
12	7	70.0	8	10	US-09-798-927-67		Sequence 67, Appli
13	7	70.0	8	10	US-09-795-847-67		Sequence 67, Appli
14	7	70.0	8	10	US-09-794-743-67		Sequence 67, Appli
15	7	70.0	8	10	US-09-794-748-67		Sequence 67, Appli
16	7	70.0	8	10	US-09-794-925-67		Sequence 67, Appli
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18	7	70.0	9	12	US-10-016-117-6		Sequence 6, Appli
19	7	70.0	10	9	US-09-865-294-69		Sequence 69, Appli

ALIGNMENTS

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RESULT 1
US-09-795-903A-4
; Application US/09795903A
; Patent No. US2002164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J. N.
; APPLICANT: Lin, Xinlin
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: or Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; SEQ ID NO 4
; SOFTWARE: PatentIn Ver. 2.1
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-795-903A-4
Query Match Score: 80.0%
Best Local Similarity: 100.0%
Matches: 8; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
Qy 1 VKMDAEFR 8
Db 3 VRMDAEFR 10
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RESULT 2
US-09-794-927-64
; Sequence 64, Application US/09794927
; Patent No. US2001016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Pardi, Luis A.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/62BDFG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic

Query Match 80.0%; Score 8; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFR 8
Db 111111
3 VKMDAEFR 10

RESULT 4
US-09-794-743-64
; Sequence 64, Application US/09794743
; Patent No. US2001002391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Pardi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/62B0BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic

Query Match 80.0%; Score 8; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFR 8
Db 111111
3 VKMDAEFR 10

RESULT 5
US-09-794-748-64
; Sequence 64, Application US/09794748
; Patent No. US2002003715A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Pardi, Luis A.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/62B0DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0

TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIORITY NUMBER: 09/416,901
; PRIOR APPLICATION NUMBER: 1999-10-13
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-748-64

Query Match Score 8; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKMDAEFR 8
Db 3 VKMDAEFR 10

RESULT 6
US-09-796-264-4
; Sequence 4, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRF 179
; CURRENT FILING DATE: 2001-02-28
; PRIORITY NUMBER: 09/614,608
; PRIOR FILING DATE: 2000-06-27
; PRIORITY NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIORITY NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIORITY NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIORITY NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-796-264-4

Query Match Score 8; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-09-794-925-64
; Sequence 64, Application US/09794925
; Patent No. US20020061819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND U
; FILE REFERENCE: 28341/6280H1
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIORITY NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIORITY NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-24
; PRIORITY NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-64

Query Match Score 8; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKMDAEFR 8
Db 3 VKMDAEFR 10

RESULT 8
US-09-881-442-64
; Sequence 64, Application US/09681442
; Patent No. US2002008163A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND U
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIORITY NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIORITY NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIORITY NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1998-09-24
; PRIORITY NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73

Qy 1 VKMDAEFR 8
Db 3 VKMDAEFR 10

; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 64
 ; LENGTH: 10
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-09-681-442-64

Query Match 80.0%; Score 8; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKMDAEFR 8
 Db 3 VKMDAEFR 10

RESULT 9
 US-09-845-226-4
 ; Sequence 4, Application US/09845226
 ; Patent No. US200115600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Jordan J.N.
 ; APPLICANT: Hong, Lin
 ; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
 ; FILE REFERENCE: OMRF 182
 ; CURRENT APPLICATION NUMBER: US/09/845,226
 ; CURRENT FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 09/603,713
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: 60/168,060
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: 60/177,836
 ; PRIOR FILING DATE: 2000-01-15
 ; PRIOR APPLICATION NUMBER: 60/178,368
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: 60/210,292
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 4
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-845-226-4

Query Match 80.0%; Score 8; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKMDAEFR 8
 Db 3 VKMDAEFR 10

RESULT 10
 US-10-057-505-10
 ; Sequence 10, Application US/10057505
 ; Patent No. US2002164474A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 ; APPLICANT: AURORA BIOSCIENCES CORPORATION
 ; APPLICANT: TSIEN, Roger
 ; APPLICANT: HEIM, Roger
 ; APPLICANT: CUBITT, Andrew
 ; TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
 ; FILE REFERENCE: REGEN1260-3
 ; CURRENT APPLICATION NUMBER: US/10/057,505
 ; CURRENT FILING DATE: 2002-01-25

Query Match 80.0%; Score 8; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKMDAEFR 8
 Db 3 VKMDAEFR 10

RESULT 11
 US-09-867-847-5
 ; Sequence 5, Application US/09867847
 ; Patent No. US2002009433A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chalifour, Robert
 ; APPLICANT: Hebert, Lise
 ; APPLICANT: Hong, Xiangqi
 ; APPLICANT: Gerans, Francine
 ; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASE RELATED DISEASES
 ; FILE REFERENCE: 14445-501 CIP
 ; CURRENT APPLICATION NUMBER: US/09/867,847
 ; CURRENT FILING DATE: 2001-09-20
 ; PRIOR APPLICATION NUMBER: 60/168,594
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/724,842
 ; PRIOR FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 5
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
 ; OTHER INFORMATION: or peptidometics

US-09-867-847-5

Query Match 70.0%; Score 7; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 VKMDAEFR 7

RESULT 12
 US-09-794-927-67
 ; Sequence 67, Application US/09794927
 ; Patent No. US200101632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Blenkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 ; TITLE OF INVENTION: USES

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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; US-09-794-927-67

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Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-09-795-847-67
; Sequence 67, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; US-09-795-847-67

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Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-09-794-743-67
; Sequence 67, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; US-09-794-743-67

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
US-09-794-748-67
; Sequence 67, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; US-09-795-847-67

Query Match 70.0%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-748-67

Query Match 70.0%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.ee+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	2	VKMDAEL	8

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Job time : 12 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:39:48 ; Search time 11.5 Seconds
 (without alignments)
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{ Title: US-09-580-018-6
 Sequence: 1 VKMDAEFRHD 10

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 Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

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Minimum DB seq length: 5
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Post processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1		80.0	10	4	US-09-548-372D-64	Sequence 64, Appl
2		80.0	10	4	US-09-548-367D-64	Sequence 64, Appl
3		70.0	7	2	US-08-792-553-10	Sequence 10, Appl
4		70.0	8	4	US-09-548-372D-67	Sequence 67, Appl
5		70.0	8	4	US-09-548-367D-67	Sequence 67, Appl
6		70.0	9	3	US-08-982-221	Sequence 221, Appl
7		70.0	9	4	US-09-294-987-6	Sequence 6, Appl
8		70.0	10	1	US-08-371-930-12	Sequence 12, Appl
9		70.0	10	2	US-08-025-321C-1	Sequence 1, Appl
10		70.0	10	5	PCT-US94-01712-12	Sequence 12, Appl
11		50.0	5	1	US-08-480-498-1	Sequence 1, Appl
12		50.0	5	2	US-08-422-333-7	Sequence 7, Appl
13		50.0	5	4	US-08-660-533-13	Sequence 13, Appl
14		50.0	5	6	5187153-6	Sequence 1, Appl
15		50.0	5	6	5220013-6	Patent No. 5187153
16		50.0	5	6	5223482-6	Patent No. 5223482
17		50.0	5	6	522482-6	Patent No. 522482
18		50.0	10	1	US-07-766-351-1	Sequence 1, Appl
19		50.0	10	1	US-08-059-032-1	Sequence 19, Appl
20		50.0	10	2	US-08-659-984A-19	Sequence 19, Appl
21		50.0	10	4	US-08-660-531-19	Sequence 63, Appl
22		50.0	10	4	US-08-440-423-4	Sequence 1, Appl
23		50.0	10	4	US-08-846-444-4	Sequence 33, Appl
24		50.0	10	4	PCT-US91-07290-1	Sequence 35, Appl
25		50.0	10	5	PCT-US91-07290-1	Sequence 33, Appl
26		40.0	7	1	US-08-136-743B-33	Sequence 119, App
27		40.0	7	1	US-08-136-743B-35	Sequence 119, App

ALIGNMENTS

RESULT 1
 US-09-548-372D-64
 ; Sequence 64, Application US/09548372D
 ; Patent No. 6420534
 ; GENERAL INFORMATION:
 ; APPLICANT: GURNEY ET AL.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
 ; FILE REFERENCE: 29915/6801
 ; CURRENT APPLICATION NUMBER: US/09/548-372D
 ; PRIORITY FILING DATE: 2000-04-12
 ; PRIORITY APPLICATION NUMBER: US 60/155,493
 ; PRIORITY FILING DATE: 1999-09-23
 ; PRIORITY APPLICATION NUMBER: US 09/404,133
 ; PRIORITY FILING DATE: 1999-09-23
 ; PRIORITY APPLICATION NUMBER: PCT/US99/20881
 ; PRIORITY FILING DATE: 1998-09-23
 ; PRIORITY APPLICATION NUMBER: US 60/101,594
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 64
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 US-09-548-372D-64

Query Match 80.0% ; Score 8; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00053; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDAEFR 8
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 Db 3 VKMDAEFR 10

RESULT 2
 US-09-548-367D-64
 ; Sequence 64, Application US/09548367D
 ; Patent No. 6440658
 ; GENERAL INFORMATION:
 ; APPLICANT: GURNEY ET AL.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
 ; FILE REFERENCE: 29915/6800H
 ; CURRENT APPLICATION NUMBER: US/09/548-367D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIORITY APPLICATION NUMBER: US 60/155,493

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-367D-64

Query Match          80.0%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    1 VKMDAEEF 8
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Db    3 VKMDAEEF 10
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RESULT 3
US-08-92-553-10
; Sequence 10, Application US/08792553
; Patent No. 5981200
; GENERAL INFORMATION:
; - APPLICANT: Tsien, Roger Y.
; - APPLICANT: Helm, Roger Y.
; TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,553
; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/041001/UC 96-160-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-792-553-10

Query Match          70.0%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    1 VKMDAEEF 7
      ||||||| 7
Db    1 VKMDAEEF 7
      ||||||| 7

RESULT 4
US-09-548-372D-67
; Sequence 67, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/63801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-548-372D-67

Query Match          70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    1 VKMDAEEF 7
      ||||||| 7
Db    2 VKMDAEEF 8
      ||||||| 8

RESULT 5
US-09-548-367D-67
; Sequence 67, Application US/09548367D
; Patent No. 6440688
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-548-367D-67

Query Match          70.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
 US-08-802-981-221
 ; Sequence 221, Application US/08802981
 ; GENERAL INFORMATION:
 ; APPLICANT: Komoriya, Akira
 ; APPLICANT: Packard, Beverly S.
 ; TITLE OF INVENTION: Compositions for the Detection of Enzyme Activity in Biological Samples and Methods of use Thereof
 ; NUMBER OF SEQUENCES: 231
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/802,981
 ; FILING DATE: 20-FEB-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunter, Tom
 ; REFERENCE/DOCKET NUMBER: 38,498
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 221:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-802-981-221

Query Match 70.0% Score 7; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKMDAEC 7
 Db 2 VKMDAEC 8

RESULT 7
 US-09-294-987-6
 ; Sequence 6, Application US/09294987
 ; GENERAL INFORMATION:
 ; APPLICANT: HOOK, Vivian Y.H.
 ; FILE REFERENCE: P-AS 3515
 ; CURRENT APPLICATION NUMBER: US/09/294,987
 ; CURRENT FILING DATE: 1999-04-20
 ; PRIOR APPLICATION NUMBER: US 09/173,887
 ; PRIOR FILING DATE: 1998-10-16
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 9

Query Match 70.0% Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0083;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKMDAEC 7
 Db 3 VKMDAEC 9

RESULT 9
 US-08-025-321C-1
 ; Sequence 1, Application US/08025321C
 ; GENERAL INFORMATION:
 ; APPLICANT: Abraham Ph.D., Carmela R.
 ; TITLE OF INVENTION: PROTEASES CAUSING ABNORMAL DEGRADATION OF AMYLOID BETA-PROTEIN PRECURSOR

NUMBER OF SEQUENCES: 13
; PRIORITY/ADDRESS: ;
; ADDRESSEES: Choate, Hall & Stewart
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/025,321C
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell, Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0079571-0034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 248 5000
; TELEFAX: 617 248 4000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-025-321C-1

RESULT 11
PCT-US94-01712-12
; sequence 12, Application PC/TUS9401712
; Query Match Score 7; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0.0083;
; Matches 7; Conservative 0; Mismatches 0; Indels 0;
; Gaps 0;

Qy 1 VKMDAEC 7
Db 4 VKMDAEC 10

RESULT 10
PCT-US94-01712-12
; sequence 12, Application PC/TUS9401712
; General Information:
; APPLICANT: Nishimoto, IKUO
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01712
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:

Query Match Score 7; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 VKMDA 5
Db 1 VKMDA 5

RESULT 12

US-08-422-333-7
; Sequence 7, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; TELEFAX: (415) 968-2438
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-422-333-7

Query Match 50.0% Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKMDA 5
Db 1 VKMDA 5

RESULT 14
US-08-660-531-13
; Sequence 13, Application US/08660531
; Patent No. 6211645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 15,270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2422
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

RESULT 13
US-08-659-984A-13
; Sequence 13, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE:

i : MOLECULE TYPE: peptide
 US-08-660-531-13

Query Match Score 5; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indexes 0;
 Gaps 0;

Qy 1 VKMDA 5
 Db 1 VKMDA 5

RESULT 15
 US-09-054-334-1
 ; sequence 1, Application US/09054334

{ GENERAL INFORMATION:

APPLICANT: Anderson, John P.
 APPLICANT: Jacobson-Croak, Kirsten L.

APPLICANT: Siania, Sukanto
 TITLE OF INVENTION: Assays for Detecting Beta-Secretase

TITLE OF INVENTION: Inhibition

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/054,334

FILING DATE: 02-APR-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,152

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 015270-002820US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-054-334-1

Query Match Score 5; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indexes 0;
 Gaps 0;

Qy 1 VKMDA 5
 Db 1 VKMDA 5

Search completed: April 21, 2003, 12:43:00
 Job time : 12.5 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 12:37:02 ; Search time 29.5 Seconds

(without alignments)
45.170 Million cell updates/sec

Title: US-09-580-018-6
Perfect-score: 10
Sequence: 1 VKMDAEFRHD 10

Scoring table: ORIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 162749

Minimum DB seq length: 5

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

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- 4: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1983.DAT:*
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- 21: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	10	100.0	10	22	AAB46210		Human APP derived
2	9	90.0	10	22	AAB46209		Human APP derived
3	9	90.0	10	22	AAB46211		Human APP derived
4	8	80.0	10	13	AAR24261		Human amyloid pr
5	8	80.0	10	21	AYY62703		Beta-APP alpha-sec
6	8	80.0	10	22	AAE1654		Human wild-type AP
7	8	80.0	10	22	AAE02899		Human amyloid prc
8	8	80.0	10	22	AAU06228		AS2 recognition s
9	8	80.0	10	22	AAU06227		Human beta-amyloid
10	80.0	80.0	10	22	AAE02606		Human wild-type AP

ALIGNMENTS

RESULT 1

AAB46210 standard; peptide: 10 AA.

ID AAB46210

XX DT 04-APR-2001 (first entry)

DE Human APP derived immunogenic peptide #6.

AC AAB46210;

XX XX

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;

KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective; KW amyloid precursor protein; Alzheimer's disease.

XX XX

OS Homo sapiens.

XX XX

PN WO200072880-A2.

PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US14810.

XX PR 28-MAY-1999; 99US-0322289.

XX PA (NBUR-) NEURALAB LTD.

PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

DR WPI; 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits, PT especially Alzheimer's disease, comprises administering amyloid specific antibody -

XX Disclosure; Figure 19; 143pp; English.
 PS This invention describes a novel method of preventing or treating a
 XX disease associated with amyloid deposits in the brain of a patient, which comprises
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it; (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunotherapy. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX

SQ Sequence 10 AA;

Query Match	Score 10;	DB 22;	Length 10;
Best Local Similarity	Pred. No. 1.5e-05;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;

Qy 1 VRMDAERHD 10

Db 1 VRMDAERHD 10

:

RESULT 2
 AAB46209

ID AAB46209 standard; Peptide; 10 AA.

XX AC AAB46209;

XX DT 04-APR-2001 (first entry)

XX DE Human APP derived immunogenic peptide #5.

XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;

CC KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;

CC KW amyloid precursor protein; Alzheimer's disease.

XX Homo sapiens.

OS WO200072880-A2.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US14810.

XX PR 28-MAY-1999; 99US-0322289.

XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX XX Disclosure; Figure 19; 143pp; English.

XX DR 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits,

PT especially Alzheimer's disease, comprises administering amyloid

PT specific antibody -

XX PS Disclosure; Figure 19; 143pp; English.

XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX XX DR 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits,

PT especially Alzheimer's disease, comprises administering amyloid

PT specific antibody -

XX PS Disclosure; Figure 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it; (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have nootropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunotherapy. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX

CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunotherapy. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

XX Sequence 10 AA;

Query Match	Score 9;	DB 22;	Length 10;
Best Local Similarity	Pred. No. 0.00023;		
Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;
			Gaps 0;

Qy 1 VRMDAERHD 9

Db 2 VRMDAERHD 10

:

RESULT 3
 AAB46211

ID AAB46211 standard; peptide; 10 AA.

XX AC AAB46211;

XX DT 04-APR-2001 (first entry)

XX DE Human APP derived immunogenic peptide #7.

XX KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;

CC KW FC receptor mediated phagocytosis; immunogenic response; neuroprotective;

CC KW amyloid precursor protein; Alzheimer's disease.

XX Homo sapiens.

OS WO200072880-A2.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US14810.

XX PR 28-MAY-1999; 99US-0322289.

XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX XX DR 2001-032104/04.

XX PT Preventing or treating a disease associated with amyloid deposits,

PT especially Alzheimer's disease, comprises administering amyloid

PT specific antibody -

XX PS Disclosure; Figure 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a

CC disease associated with amyloid deposits of amyloid precursor protein

CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the

CC antibody binds to an amyloid deposit and induces a clearing response (Fc

CC receptor mediated phagocytosis) against it; (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of

CC Abeta. The products of the invention have nootropic and neuroprotective

CC activity. The method is also useful for monitoring a course of treatment

CC being administered to a patient e.g. active and passive immunotherapy. The

CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.

XX

Query Match Score 9; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 9; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 2 KMDAERHD 10

Db	1	KMDAEFRHDS	9		XX	Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;	
RESULT 4							
AAR24261	ID	AAR24261	standard;	Protein;	10 AA.	KW cleavage site; beta-secretase; neurodegenerative disease;	
XX	AC	AAR24261;				KW Alzheimer's disease.	
XX	XX	XX	XX			XX	
DT	09-NOV-1992	(first entry)				OS Homo sapiens.	
XX	DE	Human amyloidin protease substrate sequence #1.				PN WO9964587-A1.	
XX	KW	Alzheimer's disease; beta amyloid precursor protein; APP; zinc;				XX 16-DEC-1999.	
XX	KW	metallopeptidase; hAP; protease inhibitor; APP392-601				XX 04-JUN-1999;	
OS	Synthetic.					XX 99WO-FR01326.	
XX	FH	Key				XX 05-JUN-1998;	
XX	FT	Modified-site	Location/Qualifiers			PR 98FR-0007068.	
XX	FT		/note= "Acetylated-ser"			PR 31-MAR-1999;	
XX	PN	WO207068-A.				XX 99US-0122599.	
XX	PS	WPI:	2000-097537/A8.			XX (RHON) RHONE-POULENC RORER SA.	
XX	PD	30-APR-1992.				PA (UYPK) UNIV CURIE PARIS VI P & M.	
XX	XX	XX				XX Rholam M, Munoz-Gimenez N, Moutouaukil M, Cohen P, Bertrand P;	
PF	04-OCT-1991;	91WO-US07290.				XX DR 2000-097537/A8.	
XX	PR	05-OCT-1990;	90US-0594122.			XX PS Example 3; Page 24; 44pp; French.	
XX	PR	30-SEP-1991;	91US-076351.			XX Peptides MAY69702-Y69718 represent synthetic peptide substrates for a	
XX	PA	(ATHE-) ATHENA NEUROSCIENCES INC.				CC novel polypeptide with beta-secretase activity that can cleave	
XX	PA	(ELIIL) LILLY & CO ELI.				CC specifically the natural beta-amyloid precursor protein (bAPP). Normal	
XX	PI	Dovey HF, Johnstone EM, Little SP, McConlogue L, Seubert PA;				CC cleavage of the protein occurs between amino acids Met596-Asp597 and	
PI	PI	Pi Sinha S;				CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel	
XX	DR	WPI: 1992-167148/20.				CC polypeptide is used to identify agents that interact specifically with	
XX	SQ	Human amyloidin protease - used for cleaving Met-Asp bond in				CC it. These agents regulate metabolism of APP, particularly they slow down	
PT	PT	amyloid-like substrate for identifying protease inhibitors				CC or reduce production of beta amyloid, so can be used to treat	
XX	PS	Claim 1; Page 52; 62pp; English.				CC neurodegenerative diseases, particularly Alzheimer's disease.	
XX	XX					XX Sequence 10 AA;	
CC	CC	Claimed human amyloidin protease is defined by its ability to				Query Match Score 8; DB 21; Length 10;	
CC	CC	cleave the Met-Asp bond of this synthetic substrate. The substrate,				Best Local Similarity 100.0%; Pred. No. 0.0034;	
CC	CC	which corresponds to residues 592 to 601 of the 695 amino acid APP,				Mismatches 0; Indels 0; Caps 0;	
CC	CC	can be used in an assay for identifying inhibitors of proteases				QY 1 VKMDAEFR 8	
CC	CC	which cleave Met-Asp bonds, e.g. amyloidin, human skin chymase or				Db 3 VKMDAEFR 10	
CC	CC	rat mast cell protease I or II.				RESULT 6	
CC	CC	See AAR24260-3, AAR24266-7 and AAO244875-Q244887.				AAE10654	
XX	SQ	Sequence 10 AA;				ID AAE10654 standard; peptide; 10 AA.	
Query Match Score 8; DB 13; Length 10;						XX AC AAE10654;	
Best Local Similarity 100.0%; Pred. No. 0.0034;						XX DT 10-DEC-2001 (first entry)	
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						XX Human wild-type APP beta-secretase peptide, PHA-95812E.	
QY 1 VKMDAEFR 8						XX KW Human; aspartyl protease 1; Aspl; amyloid precursor protein;	
						XX KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;	
Db 3 VKMDAEFR 10						XX KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;	
XX	XX					XX KW APP beta-secretase peptide.	
XX	XX					XX Homo sapiens.	
XX	XX					XX Key FT Cleavage-site	
XX	AC	AY69703				XX Location/Qualifiers	
XX	XX	DT 11-APR-2000 (first entry)				XX GB2357767-A.	
XX	DE	Beta-APP alpha-secretase substrate [KMD]-APP(-5,+5).				XX PD 04-JUL-2001.	

PF 22-SEP-2000; 2000GB-0023315.
 XX 19-JUL-2001.
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20081.
 PR 13-OCT-1999; 99US-0416801.
 PR 06-DEC-1999; 99US-0169332.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX Bienkowski MJ, Gurney M;
 PT DR; 2001-44208/48.
 PT Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 disease -
 XX Example 12; Page 84; 187PP; English.
 XX The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
 CC Asp1 proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Asp1 alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Asp1 alpha-secretase activity, where modulators that increase
 CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
 CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
 CC the substrate and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is wild-type
 CC human amyloid precursor protein (APP) beta-secretase specific
 CC substrate peptide, PHA-95812E. This peptide is used for assaying
 CC the beta-secretase activity of human Aspartyl protease 2a (Asp2a)
 CC protein. The peptide is also used for determining the relationship
 CC between Aspartyl protease 1 (Asp1) and APP protein.
 XX Sequence 10 AA:
 SQ Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 AC
 QY 1 VKMDAEFR 8
 ||||| | | |
 DB 3 VKMDAEFR 10
 RESULT 7
 AAE06899 ID AAE06899 standard; peptide; 10 AA.
 XX DT 23-OCT-2001 (first entry)
 DE Human amyloid precursor protein wild-type beta-secretase peptide.
 XX KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
 KW neuroprotective; antisense therapy; gene therapy.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Cleavage-site 5..6
 XX PN WO200150829-A2.

XX Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 AC
 QY 1 VKMDAEFR 8
 ||||| | | |
 DB 3 VKMDAEFR 10
 RESULT 8
 AAU06628 ID AAU06628 standard; peptide; 10 AA.
 XX AC AAU06628;
 AC ANU06628;
 XX DT 24-OCT-2001 (first entry)
 DE Asp2 recognition site from wild-type APP.
 XX KW Aspartyl protease; Asp2; beta-secretase; nootropic;
 KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
 KW amyloid-beta; Abeta.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Cleavage-site 5
 XX PN /label= Asp2_protease_cleavage_site

PN WO200149098-A2.
 XX
 PD 12-JUL-2001.
 XX
 PF 09-MAY-2001; 2001WO-IB00798.
 XX
 PR 09-MAY-2001; 2001WO-IB00798.
 XX
 PA (BIEN/) BIENKOWSKI M. J.
 PA (GURN/) GURNEY M. E.
 PA (HEIN/) HEINRIKSON R. L.
 PA (PARO/) PARODI L. A.
 PA (YANR/) YAN R.
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX
 DR WPI; 2001-502549/55.
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX
 PS Claim 127; Page 101; 185pp; English.
 XX
 CC The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp
 CC protein and vectors expressing them, and a polypeptide (isoform of
 CC an amyloid protein precursor (APP)) comprising the amino acid sequence of an
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
 CC is associated with increased levels of Abeta processing is useful in
 CC assays relating the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridise to
 CC APP oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is a peptide substrate
 CC for Asp2 corresponding to the wild-type APP beta-secretase site.
 XX
 Sequence 10 AA;
 SQ Query Match Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAEFR 8
 1|||||
 Db 3 VKMDAEFR 10
 RESULT 9
 AAE07227 standard; Peptide; 10 AA.
 XX
 ID AAE07227;
 AC AAE02606
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human beta-amyloid protein precursor, App-beta40 and 42 secretase site.
 XX
 KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease; APP-beta40; APP-beta42.
 XX
 OS Homo sapiens.
 XX
 PN WO200149097-A2.
 XX
 PD 12-JUL-2001.
 XX
 PF 09-MAY-2001; 2001WO-IB00797.
 XX
 PR 09-MAY-2001; 2001WO-IB00797.
 XX
 PA (BIEN/) BIENKOWSKI M. J.
 PA (GURN/) GURNEY M. E.
 PA (HEIN/) HEINRIKSON R. L.
 PA (PARO/) PARODI L. A.
 PA (YANR/) YAN R.
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX
 DR WPI; 2001-502548/55.
 XX
 Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX
 PS Claim 127; Page 101; 185pp; English.
 XX
 The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognisable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity, identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease, and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, APP-beta40
 CC and APP-beta42 secretase sites.
 XX
 Sequence 10 AA;
 SQ Query Match Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VKMDAEFR 8
 1|||||
 Db 3 VKMDAEFR 10
 RESULT 10
 AAE02606
 ID AAE02606 standard; Peptide; 10 AA.
 XX
 AC AAE02606;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human wild-type APP beta-secretase substrate peptide, PHA-95812E.
 XX

KW	Human; alpha-secretase; amyloid precursor protein; APP; therapy;	PF	27-JUN-2000; 2000WO-US17742.
KW	Alzheimer's disease; anti-alzheimer's; aspartyl protease 2a; Asp2a;	XX	28-JUN-1999; 99US-0141363.
KW	beta-secretase.	PR	30-NOV-1999; 99US-0168060.
OS	Homo sapiens.	PR	25-JAN-2000; 2000US-0177336.
XX		PR	27-JAN-2000; 2000US-0178368.
FH		PR	08-JUN-2000; 2000US-0210222.
FT		XX	
Key	Location/Qualifiers	PA	(OKLA-) OKLAHOMA MEDICAL RES FOUND.
Cleavage-site	5..6	PA	(UNII) UNIV ILLINOIS FOUND.
XX	WO200123533-A2.	PA	
PN		XX	
XX	05-APR-2001.	PI	Tang JJN, Hong L, Ghosh AK;
PD		XX	
XX	22-SEP-2000; 2000WO-US26080.	DR	DR WI; 2001-137933/14.
PR		XX	
XX	23-SEP-1999; 99US-0155493.	PT	Novel memapsin 2 inhibitors which bind to active site of memapsin 2
PR	23-SEP-1999; 99WO-US020881.	PT	having 2 catalytic aspartic residues and substrate binding cleft; used
PR	13-OCT-1999; 99US-0416901.	PT	to treat Alzheimer's disease by blocking amyloid precursor protein
PR	06-DEC-1999; 99US-0169232.	cleavage	
XX		XX	
PA	(PHAA-) PHARMACIA & UPJOHN CO.	PS	Disclosure; Page 11; 86pp; English.
XX		XX	
PI	Gurney M, Blenkowski MJ;	CC	The present sequence is given in a specification relating to an inhibitor
XX		CC	of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
DR	WPI; 2001-290516/30.	CC	active site, which is defined by the presence of two catalytic aspartic
XX		CC	residues and a substrate binding cleft. The inhibitor is useful for
PT	Enzymes that cleave the alpha-secretase site of the amyloid precursor	CC	the treatment and diagnosis of Alzheimer's disease. It is useful in
protein, useful for the treatment of Alzheimer's disease -		CC	screens for individuals with a genetic predisposition to Alzheimer's
PS	Example 12; Page 85; 189pp; English.	CC	disease. The inhibitor is useful as a reagent for specifically binding to
XX		CC	memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2
CC	The present invention relates to enzymes for cleaving the alpha-	CC	isolation, purification and characterisation.
secretase site of the amyloid precursor protein (APP) and methods of		XX	
CC	identifying those enzymes. The methods may be used to identify enzymes	SQ	Sequence 10 AA;
CC	that may be used to cleave the alpha-secretase cleavage site of the APP	Query Match	Score 8; DB 22; Length 10;
CC	protein. The enzymes may be used to treat or modulate the progress of	Best Local Similarity	100.0%; Pred. No. 0.0034;
CC	Alzheimer's disease. The present sequence is human wild-type amyloid	Matches	Mismatches 0; Indels 0; Gaps 0;
CC	precursor protein (APP) beta-secretase specific substrate peptide,	Qy	1 VKMDAEFR 8
CC	PHA-95812E. This peptide is used for assaying the beta-secretase activity	Db	1
CC	of human Aspartyl protease 2a (Asp2a) protein. The peptide is also used		3 VKMDAEFR 10
CC	for determining the relationship between Aspartyl protease 1 (Asp1) and		
CC	APP protein.		
XX	Sequence 10 AA;		
SQ		RESULT 12	AAB46208
	Query Match	ID	AAB46208 standard; peptide; 10 AA.
	Best Local Similarity	XX	
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC	AAB46208;
Qy	1 VKMDAEFR 8	XX	
DB	3 VKMDAEFR 10	DT	04-APR-2001 (first entry)
		XX	
		DE	Human APP derived immunogenic peptide #4.
		XX	
		XX	
		AC	WO200072880-A2.
		XX	
		DT	12-APR-2001 (first entry)
		XX	
		DE	Synthetic peptide derived from APP beta-secretase site.
		XX	
		ID	AAB6574 standard; Peptide; 10 AA.
		XX	
		AC	AAB6574;
		XX	
		DT	12-APR-2001 (first entry)
		XX	
		DE	Synthetic peptide derived from APP beta-secretase site.
		XX	
		KW	Memapsin 2; nootropic; neuroprotective; amyloid precursor protein;
		KW	APP; memapsin 2 inhibitor; Alzheimer's disease.
		XX	
		OS	synthetic.
		XX	
		PN	WO200100665-A2.
		XX	
		PD	04-JAN-2001.
		XX	
		DR	DR WI; 2001-032104/04.
		XX	

PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody .

XX Disclosure; Figure 19; 143pp; English.

PS This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP). Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it; (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

XX Sequence 10 AA;

Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKMDAERF 8
 Db 3 VKMDAERF 10
 Sq Sequence 10 AA;

RESULT 13
 AAB46212

ID AAB46212 standard; peptide; 10 AA.
 XX
 AC AAB46212;

XX DT^r
 XX 04-APR-2001 (first entry)

DE Human APP derived immunogenic peptide #8.
 XX
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.

XX OS Homo sapiens.

XX PN WO200072880-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US11810.

XX PR 28-MAY-1999; 99US-0322289.

XX PA (NEUR-) NEURALAB LTD.

XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX DR 2001-032104/04.

PS Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody .

XX Disclosure; Figure 19; 143pp; English.

PS This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP). Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing

CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

SQ Sequence 10 AA;

Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MDAAFRHD 10
 Db 1 MDAAFRHD 8

RESULT 14
 AAB61336

ID AAB61336 standard; peptide; 10 AA.
 XX
 AC AAB61336;

XX DT 02-APR-2001 (first entry)
 XX DE Synthetic peptide from beta amyloid precursor protein.
 XX KW Memapsin 2; catalyst; Alzheimer's.
 XX KW Unidentified.

OS OS
 XX PN WO200100663-A2.

XX PD 04-JAN-2001.

XX PF 27-JUN-2000; 2000WO-US17661.

XX PR 28-JUN-1999; 99US-0141363.
 PR 30-NOV-1999; 99US-0168060.
 PR 25-JAN-2000; 2000US-0177836.
 PR 27-JAN-2000; 2000US-0178368.
 PR 08-JUN-2000; 2000US-0210292.

XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX PI Tang JUN, Lin X, Koelsch G;
 XX DR 2001-102885/11.

XX PT Purified recombinant catalytically active memapsin 2, used to screen
 PT inhibitors of it, which are used to treat and prevent Alzheimer's
 PT disease -
 XX PS Claim 6; Page 11; 86pp; English.
 XX CC The present invention relates to a purified recombinant
 CC catalytically active memapsin 2. The invention may be used for
 CC isolating inhibitors which are used to treat or prevent
 CC Alzheimer's disease. The invention may also be used to screen
 CC for individuals more genetically prone to develop Alzheimer's
 CC disease.

SQ Sequence 10 AA;

Query Match 80.0%; Score 8; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VKMDAERF 8
 Db 3 VKMDAERF 10

RESULT 15
 AAU99490 standard; peptide; 10 AA.
 ID AAU99490
 XX
 AC AAU99490;
 XX DT 07-OCT-2002 (first entry)
 XX DE Peptide #1 used as substrate for human memapsin 2.
 XX PR Human; memapsin 2; beta secretase; aspartic protease; APP; beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease; neuroprotective; nootropic.
 XX KW
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN US2002049303-A1.
 XX PD 25-APR-2002.
 XX PF 28-FEB-2001; 2001US-0796264.
 XX PR 28-JUN-1999; 99US-14133P.
 PR 30-NOV-1999; 99US-168030P.
 PR 25-JAN-2000; 2000US-177836P.
 PR 27-JAN-2000; 2000US-178388P.
 PR 27-JUN-2000; 2000US-0604608.
 XX PA (TANG J /) TANG J J N.
 PA (LINKX /) LIN X.
 PA (KOELSCH G. /) KOELSCH G.
 PA (HONG L. /) HONG L.
 XX PI Tang JJN, Lin X, Koelsch G, Hong L;
 XX DR 2002-507280/54.
 XX PT New recombinant catalytically active memapsin 2, useful to screen for inhibitors of memapsin 2 which can be used to prevent and treat Alzheimer's disease.
 XX PS Claim 6; Page 30; 44pp; English.
 XX CC The present invention relates to methods for the production of purified, recombinant catalytically active, memapsin 2 (beta secretase). Memapsin 2, a member of the aspartic protease family, cleaves beta-amyloid precursor protein (APP) found in amyloid plaques. The recombinant memapsin 2 is useful for identifying inhibitors of memapsin 2 in the design of drugs for the treatment and/or prevention of Alzheimer's disease. The recombinant memapsin 2 can be used to immunise against Alzheimer's disease. The present sequence represents a peptide used as a substrate for human memapsin 2.
 XX SQ Sequence 10 AA;

Query	Match	Score	DB	Length	No.	Mismatches	Indels	Gaps	O;
Qy 1	VKMDAERF 8	80.0%	23	10;					
Db 3	VKMDAERF 10	100.0%	23	10;	0	0	0	0	0;

Search completed: April 21, 2003, 12:40:44
 Job time : 30.5 secs

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OM protein - protein search, using SW model

Run on: April 21, 2003, 12:03:55 ; Search time 28 Seconds
(without alignments)
(309.071 Million cell updates/sec)

Title: US-09-580-018-42

Perfect score: 217

Sequence: 1 DAEFRHDSGYEVHKVLVFF.....DVGSNKGAIIGLMVGGVIA 42

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen Parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SptREMBL_21;*

1: sp_archaea;*

2: sp_bacteria;*

3: sp_fungi;*

4: sp_invertebrate;*

5: sp_human;*

6: sp_invertebrate;*

7: sp_mhc;*

8: sp_organelle;*

9: sp_prokaryote;*

10: sp_plant;*

11: sp_rabbit;*

12: sp_virus;*

13: sp_vertebrate;*

14: sp_unclassified;*

15: sp_virus;*

16: sp_bacteriophage;*

17: sp_archeap;*

ALIGNMENTS

17 198 91.2 747 13 991963
18 195 89.9 695 13 998sf9
19 188 86.6 699 13 07394
20 176 81.1 33 4 Q9UC33
21 175 80.6 780 13 073683
22 171 78.8 737 13 093279
23 162 74.7 30 4 Q9UCA9
24 157.5 72.6 357 13 08UUI8
25 157.5 72.6 472 13 09UUS0
26 157.5 72.6 612 13 09T9E7
27 156 72.6 738 13 09W028
28 156 71.9 239 13 09UUI7
29 156 71.9 694 13 08UUI9
30 147 67.7 28 4 Q9UCD1
31 121 65.8 49 6 097917
32 106 48.8 19 4 Q9UCC8
33 95 43.8 35 4 Q8WZ99
34 64 29.5 328 2 Q9RPS4
35 63 29.0 321 16 Q8RG41
36 63 29.0 755 2 09T717
37 63 29.0 755 2 Q9R472
38 63 29.0 755 2 Q9R694
39 63 29.0 755 16 Q8UGA3
40 62 28.6 755 2 Q44388
41 60 27.6 755 2 Q9WWA1
42 59 27.2 20 4 Q9UCB6
43 57.5 26.5 895 10 Q9AWB6
44 57 26.3 102662 10 Q22662
45 57 26.3 332 12 Q9DQNS

RESULT 1

Q16014 PRELIMINARY;
ID Q16014;
AC Q16014;
DT 01-NOV-1996 (TREMBL); 01, Created
DT 01-NOV-1996 (TREMBL); 01, Last sequence update
DT 01-JUN-2002 (TREMBL); 21, Last annotation update
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.
RN [1]
DR NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RX MEDLINE-9323601; PubMed=8476439;
RA Deeman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103 (1993).
EMBL: S60721; AAB6263.2;
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP.1.

FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;
Query Match Best Local Similarity 100.0%; Score 217; DB 4; Length 82;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKVLVFFADGVGSKGATIGLMVGGVIA 42
Db 18 DAEFRHDSGYEVHKVLVFFADGVGSKGATIGLMVGGVIA 59
RESULT 2
Q16019 PRELIMINARY;
ID Q16019

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	217	100.0	82	4	Q16014	Q16014 homo sapien
2	217	100.0	82	4	Q16019	Q16019 homo sapien
3	217	100.0	82	4	Q16020	Q16020 homo sapien
4	217	100.0	82	4	P78438	P78438 homo sapien
5	217	100.0	534	13	093296	093296 gallus gallus
6	217	100.0	569	13	09PVLI	09PVLI gallus gallus
7	217	100.0	6	Q95Kn7	Q95Kn7 macaca fasciata	
8	217	100.0	695	11	060496	060496 cavia sp. p
9	217	100.0	695	13	Q9dgj8	Q9dgj8 gallus gallus
10	217	100.0	751	13	Q9DGJ7	Q9dgj7 gallus gallus
11	217	100.0	770	6	Q9TU10	Q9tu10 sus scrofa
12	207	95.4	97	4	Q13778	Q13778 homo sapien
13	198	91.2	79	11	Q35463	Q35463 cricetus
14	198	91.2	607	11	Q99K32	Q99K32 mus musculus
15	198	91.2	693	13	Q98SG0	Q98sg0 xenopus laevis
16	198	91.2	695	11	P97487	P97487 mus musculus

AC	Q16019;	PRELIMINARY;	PRT;	82 AA.
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Beta amyloid peptide (Fragment).			
GN	BETA APP			
OS	Homo sapiens (Human).			
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9236661; PubMed=8476439;			
RA	Dennman R.B., Rosenzwaig R., Miller D.L.;			
RT	"A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";			
RT	Biophys. Res. Commun. 192:96-103(1993).			
RL	EMBL: S61380; AAB26264.2; -			
DR	HSSP: P05067; IBA4.			
DR	InterPro: IPR012255; Beta-APP.			
DR	PFam: PF03494; Beta-APP; 1.			
FT	NON_TER 1 1			
FT	NON_TER 82 82			
SQ	SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;			
Query Match	Best Local Similarity 100.0%; Score 217; DB 4; Length 82; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 DAEFRHDSGYEVHKLVFFAEDGVGSNKGAIIGLMVGGVVIA 42			
Db	18 DAEFRHDSGYEVHKLVFFAEDGVGSNKGAIIGLMVGGVVIA 59			
RESULT 3				
Q16020	ID Q16020 PRELIMINARY; PRT; 82 AA.			
AC	Q16020; DR 01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DE	Beta amyloid peptide (Fragment).			
GN	BETA APP			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9323601; PubMed=8476439;			
RA	Dennman R.B., Rosenzwaig R., Miller D.L.;			
RT	"A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";			
RL	Biophys. Res. Commun. 192:96-103(1993).			
DR	HSSP: P05067; IBA4.			
DR	InterPro: IPR012255; Beta-APP.			
DR	PFam: PF03494; Beta-APP; 1.			
FT	NON_TER 1 1			
FT	NON_TER 82 82			
SQ	SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;			
Query Match	Best Local Similarity 100.0%; Score 217; DB 4; Length 82; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 DAEFRHDSGYEVHKLVFFAEDGVGSNKGAIIGLMVGGVVIA 42			
Db	17 DAEFRHDSGYEVHKLVFFAEDGVGSNKGAIIGLMVGGVVIA 58			
RESULT 5				
Q93296	ID Q93296 PRELIMINARY; PRT; 534 AA.			
AC	Q93296; DR 01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DE	Amyloid protein (Fragment).			
OS	Gallus gallus (Chicken).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98337885; PubMed=9671674;			
RA	Barnes N.Y.; Li L.; Yoshikawa K.; Schwartz L.M., Oppenheim R.W., Milligan C.E.;			
RT	"Increased production of amyloid precursor protein provides a			

RT	substrate for caspase-3 in dying motoneurons.";	DE	Amyloid b-protein precursor.
RL	J. Neurosci. 18:5869-5880(1998).	OS	Macaca fascicularis; (Crab eating macaque) (Cynomolgus monkey).
DR	EMBL; AF042098; AAC25052.1; -.	OC	Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	P05067; 1BA4.	OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
DR	InterPro; IPR001898; A4_APP.	OC	Cercopithecinae; Macaca.
DR	InterPro; IPR001255; Beta-APP.	OX	NCBI_TaxID=9541;
PFam	PF02177; A4_EXTRA; 1.	[1]	RN
DR	Pfam; PF03494; Beta-APP; 1.	RP	SEQUENCE FROM N.A.
DR	PRINTS; PRO0203; AMYLOIDA4.	RC	TISSUE=CEPHALOLUM;
DR	PROSITE; PS00319; A4_EXTRA; 1.	RX	MEDLINE=91273117; PubMed=1905108;
DR	PROSITE; PS00320; A4_INTRAA; 1.	RA	InteroPro; IPR001868; A4_APP.
FT	NON_TER 1	RT	"Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease."
SQ	SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;	RT	Am. J. Pathol. 138:1423-1435(1991).
Query Match	100.0%; Score 217; DB 13; Length 534;	RL	Am. J. Pathol. 138:1423-1435(1991).
Best Local Similarity 100.0%; Pred. No. 1.8e-21;	DR	EMBL; M58727; AAA3629.1; -.	
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	InteroPro; IPR001868; A4_APP.	
DR	Q9PVLL PRELIMINARY; PRT; 569 AA.	DR	IPR001255; Beta-APP.
AC	Q9PVLL.	DR	pfam; PF02177; A4_EXTRA; 1.
DT	01-MAY-2000 (TREMBrel. 13; Created)	DR	PROSITE; PS00319; A4_EXTRA; UNKNOWN_1.
DT	01-MAY-2000 (TREMBrel. 13; Last sequence update)	DR	PROSITE; PS00320; A4_INTRAA; UNKNOWN_1.
DT	01-JUN-2002 (TREMBrel. 21; Last annotation update)	FT	SIGNAL 17 SIGNAL 17 POTENTIAL.
DE	Amyloid protein (Fragment).	FT	CHAIN 597 636 POTENTIAL.
GN	APP.	SQ	SEQUENCE 695 AA; 78663 MW; 4F6EA019F969D56 CRC64;
OS	Gallus gallus (Chicken).	RESULT 8	Q60496 PRELIMINARY; PRT; 695 AA.
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianinae;	ID	Q60496 ID 060496 PRELIMINARY; PRT; 695 AA.
OC	Gallus.	AC	Q60496 AC 060496 PRELIMINARY; PRT; 695 AA.
OX	[1]	DT	01-NOV-1996 (TREMBrel. 01; Created)
RN	SEQUENCE FROM N.A.	DT	01-NOV-1996 (TREMBrel. 01; Last sequence update)
RC	TISSUE=BRAIN;	DT	01-JUN-2002 (TREMBrel. 21; Last annotation update)
RA	Colson E.J., Paliga K., Beyreuther K., Masters C.L.;	DE	Putative amyloid precursor protein.
RT	"What the evolution of the amyloid protein precursor supergene family tells us about its function."	OS	Cavia sp.
RT	Neurochem. Int. 0:0-20000.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RL	EMBL; AF030341; AAF12698.1; -.	OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
DR	HSPP; P05067; 1BA4.	[1]	NCBI_TaxID=10143;
DR	InterPro; IPR001868; A4_APP.	RN	SEQUENCE FROM N.A.
DR	InterPro; IPR001255; Beta-APP.	RC	MEIDLINE=91236426; PubMed=9116031;
PFam	PF02177; A4_EXTRA; 1.	RA	Beck M., Mueller D., Bigl V.;
DR	PRINTS; PRO0203; AMYLOIDA4;	RT	"Amyloid precursor protein in Guinea pigs - complete cDNA sequence and alternative splicing";
DR	PROSITE; PS00319; A4_EXTRA; 1.	RT	alternative splicing";
DR	PROSITE; PS00320; A4_INTRAA; 1.	RL	Biochim. Biophys. Acta 1351:17-21(1997).
FT	NON_TER 1	DR	HSSP; P05067; 1BA4.
SQ	SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;	DR	InterPro; IPR001868; A4_APP.
Query Match	100.0%; Score 217; DB 13; Length 569;	DR	InterPro; IPR001255; Beta-APP.
Best Local Similarity 100.0%; Pred. No. 1.9e-21;	DR	pfam; PF02177; A4_EXTRA; 1.	
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	pfam; PF03494; Beta-APP; 1.	
DR	Q95KN7 PRELIMINARY; PRT; 695 AA.	DR	PRINTS; PRO0203; AMYLOIDA4.
AC	Q95KN7.	DR	SMART; SNO006; A4_EXTRA; 1.
DT	01-DEC-2001 (TREMBrel. 19; Created)	DR	PROSITE; PS00319; A4_EXTRA; 1.
DT	01-DEC-2001 (TREMBrel. 19; Last sequence update)	DR	PROSITE; PS00320; A4_INTRAA; 1.
DT	01-JUN-2002 (TREMBrel. 21; Last annotation update)	SQ	SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;
Query Match	100.0%; Score 217; DB 11; Length 695;	RESULT 7	Q95KN7 PRELIMINARY; PRT; 695 AA.
Best Local Similarity 100.0%; Pred. No. 2.4e-21;	ID	Q95KN7 ID Q95KN7 PRELIMINARY; PRT; 695 AA.	
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC	Q95KN7 AC Q95KN7 PRELIMINARY; PRT; 695 AA.	
DR	01-DEC-2001 (TREMBrel. 19; Created)	DT	01-DEC-2001 (TREMBrel. 19; Last sequence update)
DT	01-DEC-2001 (TREMBrel. 19; Last annotation update)	DT	01-DEC-2001 (TREMBrel. 21; Last annotation update)

Db	597 DAEFRHDSGYEVHHQKLVFFAEDGSNKGAIIGLMVGGVVIA 638	DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00131; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPTI_KUNITZ_1; 1. DR PROSITE; PS00279; BPTI_KUNITZ_2; 1. KW Serine protease inhibitor. SQ SEQUENCE 751 AA; E78E9413A8033D84 CRC64;
RESULT 9		
ID Q9DGJ8; AC Q9DGJ8;	PRELIMINARY; PRT; 695 AA.	Query Match 100.0%; Score 217; DB 13; Length 751; Best Local Similarity 100.0%; Pred. No. 2.7e-21; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT 01-MAR-2001 (TREMBLrel. 16, Created) DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update) DE Beta amyloid precursor protein 695 isoform.	Gallus gallus (Chicken); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. NCBI_TAXID=9031; RN [1]; RP SEQUENCE FROM N.A. RA Saras M., Rodolosse A., Sorribas V.; RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms"; RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR AF289218; AAG00593_1; -. HSSP; P05067; 1BA4. DR InterPro; IPR01868; A4_APP. DR Pfam; PE02177; A4_EXTRA; 1. Pfam; PF03494; Beta_APP; 1. DR PRINTS; PRO0205; AMYLOID4. SMART; SM00006; A4_EXTRA; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. SQ SEQUENCE 695 AA; F201ED02AEC86D95 CRC64;	DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00131; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPTI_KUNITZ_1; 1. DR PROSITE; PS00279; BPTI_KUNITZ_2; 1. KW Sequence from N.A. RA Kamura A., Takahashi T.; RT "Amyloid Precursor Protein 770"; RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. DR AB03250; BAA84580_1; -. HSSP; P05067; 1AAP. DR InterPro; IPR001255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PF02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR Pfam; PF00044; Kunitz_BPTI; 1. DR PRINTS; PRO0003; AMYLOID4. DR PRINTS; PRO0159; BASICPTASE. DR PRODOM; PD000222; Kunitz_BPTI; 1. DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00131; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPTI_KUNITZ_1; 1. DR PROSITE; PS00279; BPTI_KUNITZ_2; 1. KW Sequence from N.A. RA Saras M., Rodolosse A., Sorribas V.; RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms"; RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR AF289219; AAG00594_1; -. DR HSSP; P05067; 1BA4. DR InterPro; IPR01868; A4_APP. DR InterPro; IPR01255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PE02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR PRINTS; PRO0014; Kunitz_BPTI; 1. DR PRINTS; PRO0003; AMYLOID4. DR PRODOM; PD000222; Kunitz_BPTI; 1. DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00131; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPTI_KUNITZ_1; 1. DR PROSITE; PS00279; BPTI_KUNITZ_2; 1. KW Sequence from N.A. RA Saras M., Rodolosse A., Sorribas V.; RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms"; RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR AF289219; AAG00594_1; -. DR HSSP; P05067; 1BA4. DR InterPro; IPR01868; A4_APP. DR InterPro; IPR01255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PE02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR PRINTS; PRO0014; Kunitz_BPTI; 1. DR PRINTS; PRO00203; AMYLOID4. DR PRINTS; PRO0759; BASICPTASE. DR PRODOM; PD000222; Kunitz_BPTI; 1.
RESULT 10		
ID Q9DGJ7; AC Q9DGJ7;	PRELIMINARY; PRT; 751 AA.	Query Match 100.0%; Score 217; DB 13; Length 695; Best Local Similarity 100.0%; Pred. No. 2.4e-21; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT 01-MAR-2001 (TREMBLrel. 16, Created) DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update) DE Beta amyloid precursor protein 751 isoform.	Gallus gallus (Chicken); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. NCBI_TAXID=9031; RN [1]; RP SEQUENCE FROM N.A. RA Saras M., Rodolosse A., Sorribas V.; RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms"; RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR AF289219; AAG00594_1; -. DR HSSP; P05067; 1BA4. DR InterPro; IPR01868; A4_APP. DR InterPro; IPR01255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PE02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR PRINTS; PRO0014; Kunitz_BPTI; 1. DR PRINTS; PRO00203; AMYLOID4. DR PRINTS; PRO0759; BASICPTASE. DR PRODOM; PD000222; Kunitz_BPTI; 1.	DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00131; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPTI_KUNITZ_1; 1. DR PROSITE; PS00279; BPTI_KUNITZ_2; 1. KW Sequence from N.A. RA Saras M., Rodolosse A., Sorribas V.; RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms"; RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR AF289219; AAG00594_1; -. DR HSSP; P05067; 1BA4. DR InterPro; IPR01868; A4_APP. DR InterPro; IPR01255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PE02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR PRINTS; PRO0014; Kunitz_BPTI; 1. DR PRINTS; PRO00203; AMYLOID4. DR PRINTS; PRO0759; BASICPTASE. DR PRODOM; PD000222; Kunitz_BPTI; 1.
RESULT 11		
ID Q9TU10; AC Q9TU10;	PRELIMINARY; PRT; 770 AA.	Query Match 100.0%; Score 217; DB 13; Length 751; Best Local Similarity 100.0%; Pred. No. 2.7e-21; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-JUN-2002 (TREMBLrel. 13, Last sequence update)	Gallus gallus (Chicken); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. NCBI_TAXID=9031; RN [1]; RP SEQUENCE FROM N.A. RA Kamura A., Takahashi T.; RT Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. DR AB03250; BAA84580_1; -. HSSP; P05067; 1AAPP. DR InterPro; IPR001255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PF02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR Pfam; PF00044; Kunitz_BPTI; 1. DR PRINTS; PRO0003; AMYLOID4. DR PRINTS; PRO0159; BASICPTASE. DR PRODOM; PD000222; Kunitz_BPTI; 1. DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00131; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPTI_KUNITZ_1; 1. DR PROSITE; PS00279; BPTI_KUNITZ_2; 1. KW Sequence from N.A. RA Kamura A., Takahashi T.; RT Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. DR AB03250; BAA84580_1; -. HSSP; P05067; 1AAPP. DR InterPro; IPR001255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PF02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR Pfam; PF00044; Kunitz_BPTI; 1. DR PRINTS; PRO0003; AMYLOID4. DR PRINTS; PRO0159; BASICPTASE. DR PRODOM; PD000222; Kunitz_BPTI; 1.	DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00131; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPTI_KUNITZ_1; 1. DR PROSITE; PS00279; BPTI_KUNITZ_2; 1. KW Sequence from N.A. RA Kamura A., Takahashi T.; RT Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. DR AB03250; BAA84580_1; -. HSSP; P05067; 1AAPP. DR InterPro; IPR001255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PF02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR Pfam; PF00044; Kunitz_BPTI; 1. DR PRINTS; PRO0003; AMYLOID4. DR PRINTS; PRO0159; BASICPTASE. DR PRODOM; PD000222; Kunitz_BPTI; 1.
RESULT 12		
ID Q13778; AC Q13778;	PRELIMINARY; PRT; 97 AA.	Query Match 100.0%; Score 217; DB 6; Length 770; Best Local Similarity 100.0%; Pred. No. 2.7e-21; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT 01-NOV-1996 (TREMBLrel. 01, Created) DT 01-JUN-2002 (TREMBLrel. 01, Last sequence update)	Gallus gallus (Chicken); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. NCBI_TAXID=9031; RN [1]; RP SEQUENCE FROM N.A. RA Saras M., Rodolosse A., Sorribas V.; RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms"; RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR AF289219; AAG00594_1; -. DR HSSP; P05067; 1BA4. DR InterPro; IPR01868; A4_APP. DR InterPro; IPR01255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PE02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR PRINTS; PRO0014; Kunitz_BPTI; 1. DR PRINTS; PRO00203; AMYLOID4. DR PRINTS; PRO0759; BASICPTASE. DR PRODOM; PD000222; Kunitz_BPTI; 1.	DR SMART; SM00006; A4_EXTRA; 1. DR SMART; SM00131; KU; 1. DR PROSITE; PS00319; A4_EXTRA; 1. DR PROSITE; PS00320; A4_INTRA; 1. DR PROSITE; PS00280; BPTI_KUNITZ_1; 1. DR PROSITE; PS00279; BPTI_KUNITZ_2; 1. KW Sequence from N.A. RA Saras M., Rodolosse A., Sorribas V.; RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms"; RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. DR AF289219; AAG00594_1; -. DR HSSP; P05067; 1BA4. DR InterPro; IPR01868; A4_APP. DR InterPro; IPR01255; Beta_APP. DR InterPro; IPR002223; Kunitz_BPTI. DR Pfam; PE02177; A4_EXTRA; 1. DR Pfam; PF03494; Beta_APP; 1. DR PRINTS; PRO0014; Kunitz_BPTI; 1. DR PRINTS; PRO00203; AMYLOID4. DR PRINTS; PRO0759; BASICPTASE. DR PRODOM; PD000222; Kunitz_BPTI; 1.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.
MEDLINE=8712328; PubMed=3810169;

RX Goidgaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
"Characterization and chromosomal localization of a cDNA encoding
brain amyloid of Alzheimer's disease."
Science 235:877-880(1987).

RA HSSP; P05067; 1BA4.

RT DR InterPro; IPR001868; A4_APP.

RT DR InterPro; IPR001255; Beta-APP.

RT DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00203; AMYLOIDA4.

NON_TER 1 1

SEQUENCE 97 AA; 10844 MW; E528CDB448DE474E CRC64;

Query Match 95.4%; Score 207; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.5e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EFRHDSGEVHQLVFFAEDVGSNKGATIGLMGGVIA 42
Db 1 EFRHDSGEVHQLVFFAEDVGSNKGATIGLMGGVIA 40

RESULT 13

035463 ID PRELIMINARY; PRT; 79 AA.
AC 035463; 1

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).

GN BEA_APP.

OS Cricetulus griseus (Chinese hamster)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.

OX NCBI_TaxID=10029;

RN [1]

RP SEQUENCE FROM N.A.
Sambamurti K., Pinnix J., Gandhi S.;
Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.

RA DR EMBL; AF030413; AAB86608.1; -.

RA DR HSSP; P05067; 1BA4.

RT DR InterPro; IPR001255; Beta-APP.

RT DR Pfam; PF03494; Beta-APP; 1.

NON_TER 1 1

SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFFF3F597 CRC64;

Query Match 91.2%; Score 198; DB 11; Length 79;
Best Local Similarity 92.9%; Pred. No. 7.6e-20;
Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGEVHQLVFFAEDVGSNKGATIGLMGGVIA 42
Db 21 DAEFGHDGDFEVHQLVFFAEDVGSNKGATIGLMGGVIA 62

RESULT 14

Q99K32 ID PRELIMINARY; PRT; 607 AA.
AC Q99K32; 1

DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE DR Hypothetical 68.4 kDa protein (Fragment).

GN APP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10030;

RN [1]

RP SEQUENCE FROM N.A.
Straubring R.; Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RA DR EMBL; BC005490; AAH05490.1; -.

RT DR HSSP; P05067; 1AAP.

RT DR MGII; 88059; APP.

RT DR InterPro; IPR001868; A4_APP.

RT DR InterPro; IPR001255; Beta-APP.

RT DR InterPro; IPR00223; Kunitz_BPTI.

RT DR Pfam; PF02477; A4_EXTRA; 1.

RT DR Pfam; PF03494; Beta-APP; 1.

RT DR PRINTS; PR00203; AMYLOIDA4.

RT DR PRODOM; PD00022; Kunitz_BPTI; 1.

RT DR SMART; SM00131; KU; 1.

RT DR PROSITE; PS00319; A4_EXTRA; 1.

RT DR PROSITE; PS00320; A4_INTRA; 1.

RT DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

RT DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

KW Hypothetical protein; Serine protease inhibitor.

NON_TER 1

SEQUENCE 607 AA; 68391 MW; BF002214CBAD172 CRC64;

Query Match 91.2%; Score 198; DB 11; Length 607;
Best Local Similarity 92.9%; Pred. No. 8.8e-19;
Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGEVHQLVFFAEDVGSNKGATIGLMGGVIA 42
Db 509 DAEFGHDGDFEVHQLVFFAEDVGSNKGATIGLMGGVIA 550

RESULT 15

Q98SG0 ID PRELIMINARY; PRT; 693 AA.
AC Q98SG0; 1

RP SEQUENCE FROM N.A.
Van den Hurk W.H.

RA DR Q98SG0; 1

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Beta-amyloid precursor protein A.

GN APP.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.
Van den Hurk W.H.

RA DR Thesis (2001). Department of Biological Sciences,
University of Nijmegen, Nijmegen, Netherlands.

RL DR EMBL; AJ298150; CA37193.1; -.

DR HSSP; P05067; 1HZ3

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02477; A4_EXTRA; 1.

DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4_EXTRA; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

KW Signal.

FT SIGNAL 1 18

SEQUENCE 693 AA; 78568 MW; CA1DF55C1AB653 CRC64;

Query Match 91.2%; Score 198; DB 13; Length 693;
Best Local Similarity 88.1%; Pred. No. 1e-18;
Matches 37; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGGEVHHQKLVEVHQAEDGSNKGAIIGLMVGGVIA 42
Db 595 DSEYRHDATAXEVHHQKLVEVHQAEEGSNKGAIIGLMVGGVIA 636

Search completed: April 21, 2003, 12:07:22
Job time : 30 secs

Result No.	Query	Score	Match	Length	DB ID	Description
1	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	217	100.0	57	A4_PIG
2	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	217	100.0	57	A4_PIG
3	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	217	100.0	57	A4_PIG
4	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	217	100.0	58	A4_CANFA
5	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	217	100.0	58	A4_RABEP
6	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	217	100.0	59	A4_BOVIN
7	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	217	100.0	751	A4_SAISC
8	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	217	100.0	770	A4_HUMAN
9	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	198	91.2	770	A4_MOUSE
10	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	198	91.2	770	A4 RAT
11	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	62	28.6	755	TR2M_LGRT4
12	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	61	28.1	755	TR2N_AGRVTI
13	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	57	26.3	327	POLG_PVYCH
14	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	57	26.3	503	Y226_MICPN
15	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	56.5	25.6	378	SUG1_BEAST
16	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	55	25.6	297	FTR_ARCFU
17	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	55	25.3	488	DHAL_DSESP
18	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	55	25.3	3063	POLG_PVYN
19	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	54.5	25.1	967	PDB2_ARATH
20	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	54	24.9	284	POLG_PVYYO
21	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	53.5	24.7	708	YN2B_GAEL
22	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	53.5	24.7	971	Y228_BORBU
23	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	52	24.0	611	YCR3_BEAST
24	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	51	23.5	494	COBQ_NYCTU
25	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	51	23.5	769	ITB2_BOVIN
26	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	50.5	23.3	915	PDB2_ARATH
27	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	50	23.0	285	MENB_HAEIN
28	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	50	23.0	1437	MRP5_HUMAN
29	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	50	23.0	3579	STAN_DROME
30	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	49.5	22.8	1162	VGL2_EBV
31	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	49	22.6	1	TPIS_CULTA
32	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	49	22.6	322	Y853_RICPR
33	DAEFRHDSCYEVHQRLVFF.....DVGSNKGAILGLMGGVVIA	42	49	22.6	403	PGK_STRCO

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	Q29023 sus scrofa	57	1	57	A4_PIG	Q29023 sus scrofa
2	Q29149 ursus marit	57	1	57	A4_URSMA	Q29149 ursus marit
3	Q28280 canis famil	58	1	58	A4_CANFA	Q28280 canis famil
4	Q28748 orctocatagus	58	1	58	A4_RABEP	Q28748 orctocatagus
5	Q28757 ovis aries	58	1	58	A4_SHEEP	Q28757 ovis aries
6	Q28053 bos taurus	59	1	59	A4_BOVIN	Q28053 bos taurus
7	Q95241 salmiri sci	59	1	59	A4_SAISC	Q95241 salmiri sci
8	P05057 homo sapien	70	1	70	A4_HUMAN	P05057 homo sapien
9	P12023 mus musculu	70	1	70	A4_MOUSE	P12023 mus musculu
10	P08532 ratno norv	70	1	70	A4 RAT	P08532 ratno norv
11	P04029 agrobacteri	70	1	70	TR2M_LGRT4	P04029 agrobacteri
12	P25017 agrobacteri	70	1	70	TR2N_AGRVTI	P25017 agrobacteri
13	P21294 potamo virus	755	1	755	POLG_PVYCH	P21294 potamo virus
14	P75462 mycoplasma	755	1	755	Y226_MICPN	P75462 mycoplasma
15	P544867 sacharomyces	755	1	755	SUG1_BEAST	P544867 sacharomyces
16	O28076 archaeoglob	755	1	755	DHAL_DSESP	O28076 archaeoglob
17	P33008 pseudomonas	755	1	755	POLG_PVYN	P33008 pseudomonas
18	P18247 p genome po	763	1	763	POLG_PVYN	P18247 p genome po
19	P93753 arabiopsis	767	1	767	PDB2_ARATH	P93753 arabiopsis
20	P11897 potato virus	784	1	784	POLG_PVYYO	P11897 potato virus
21	P45972 caenorhabdi	784	1	784	YN2B_GAEL	P45972 caenorhabdi
22	P051246 borellia bu	784	1	784	TR2M_LGRT4	P051246 borellia bu
23	P25351 sacharomy	784	1	784	TR2N_AGRVTI	P25351 sacharomy
24	P053677 mycobacteri	793	1	793	COBQ_NYCTU	P053677 mycobacteri
25	P32392 bos taurus	796	1	796	ITB2_BOVIN	P32392 bos taurus
26	P23078 arabiopsis	915	1	915	PDB2_ARATH	P23078 arabiopsis
27	P145460 haemophilus	915	1	915	MENB_HAEIN	P145460 haemophilus
28	P015440 homo sapien	915	1	915	MRP5_HUMAN	P015440 homo sapien
29	P9v5n8 drosophila	915	1	915	STAN_DROME	P9v5n8 drosophila
30	P12651 avian infec	1162	1	1162	VGL2_EBV	P12651 avian infec
31	P30741 culex tarsa	1162	1	1162	TPIS_CULTA	P30741 culex tarsa
32	P9zcat9 rickettsia	1162	1	1162	Y853_RICPR	P9zcat9 rickettsia
33	P9z519 streptomyce	1162	1	1162	PGK_STRCO	P9z519 streptomyce

ALIGNMENTS

RESULT 1	STANDARD;	PRT;	57 AA.
A4_PIG			
ID Q29023;			
AC Q29023;			
DT 01-NOV-1997 (Rel. 35, Created)			
DT 01-NOV-1997 (Rel. 35, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta APP) (A-beta)] (Fragment).			
DE protein (Beta APP) (A-beta).			
GN APP.			
OS Sus scrofa (Pig).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Susina; Suidae; Sus.			
NCB_TaxID=9823;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Brain;			
RX MEDLINE=02017079; PubMed=1656157;			
RA Johnstone E.M.; Chaney M.O.; Norris F.H.; Pascual R.; Little S.P.;			
RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."			
RT Brain Res. Mol. Brain Res. 10:295-305 (1991).			
CC FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN (O) (BY SIMILARITY).			
CC SUBCELLULAR LOCATION: TYPE I membrane protein.			
CC SIMILARITY: BELONGS TO THE APP FAMILY.			
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CC EMBL: X56127; CAA19592; 1; -			
DR HSSP; P05067; 1BA4; InterPro; IPR001858; A4_APP.			
DR InterPro; IPR001255; Beta-APP.			
DR Pfam; PF03494; Beta-APP; 1.			
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.			
DR PROSITE; PS00320; A4_INTRA; PARTIAL.			
KW Glycoprotein; Amyloid; Neuron; Transmembrane.			
FT NON_TER	1	1	
FT CHAIN	6	48	BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN	<1	33	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	34	57	POTENTIAL.
FT NON_TER	57	57	
SQ SEQUENCE	57 AA;	6172 MW;	84209D88EBAB2DFA CRC64;
Query Match	100.0%	Score 217; DB 1;	Length 57;
Best Local Similarity	100.0%	Pred. No. 7.9e-22;	
Matches 42;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;			

RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
 RT Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC EMBL: X56129; CAA39594_1; -.
 CC DR HSSP; P05067; IBA4.
 CC DR InterPro; IPR001868; A4_APP.
 CC DR InterPro; IPR001255; Beta-APP.
 CC DR PF03494; Beta_APP; 1.
 CC DR PROSITE; PS00320; A4_EXTRA; PARTIAL.
 CC DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 CC KW Glycoprotein; Amyloid; Neuron; Transmembrane.
 CC FT NON_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
 CC FT CHAIN 6 48 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN <1 33 PROTEIN (POTENTIAL).
 CC FT TRANSMEM 34 57 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 CC FT NON_TER 58 58
 CC SQ SEQUENCE 58 AA; 6300 MW; F434209D8BBA82D CRC64;

Query Match 100.0%; Score 217; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 8.1e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMVGGVIA 42
 Db 6 DAEFRHDSGYEVHKLVFFAEDVGSNKGAIIGLMVGGVIA 47

RESULT 6

A4_BOVIN STANDARD; PRT; 59 AA.
 ID A4_BOVIN STANDARD; PRT; 59 AA.
 AC Q28053;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE Alzheimer's disease amyloid A4 protein homolog (Fragment).
 RN [1]
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.;
 RL Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC EMBL: X56124; CAA39591_1; -.
 CC DR X56126; CAA39591_1; -.
 CC DR InterPro; IPR001868; A4_APP.
 CC DR InterPro; IPR001255; Beta-APP.
 CC DR PF03494; Beta_APP; 1.
 CC DR PROSITE; PS00320; A4_EXTRA; PARTIAL.
 CC DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 CC KW Glycoprotein; Amyloid; Neuron; Transmembrane.
 CC FT NON_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
 CC FT CHAIN 6 48 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN <1 33 PROTEIN (POTENTIAL).
 CC FT TRANSMEM 34 57 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 CC FT NON_TER 58 58
 CC SQ SEQUENCE 58 AA; 6300 MW; F434209D8BBA82D CRC64;

RESULT 6

A4_BOVIN STANDARD; PRT; 59 AA.
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 OC NCBITAXID=9913;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.;
 RT Brain Res. Mol. Brain Res. 10:299-305(1991).
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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DR	HSSP; P05067; 1BA4;	DR	Pfam; PF03494; Beta-APP; 1.
DR	InterPro; IPR01868; A4-APP.	DR	PRINTS; PRO0203; AMYLOIDAA.
DR	InterPro; IPR01255; Beta-APP.	DR	PRINTS; PRO00759; BASICPTPE.
DR	Pfam; PF01494; Beta-APP; 1.	DR	PRODOM; PD000222; Kunitz_BPTI; 1.
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.	DR	SMART; SM00131; KU; 1.
DR	PROSTE; PS00320; A4_INTRA; PARTIAL.	DR	PROSTE; PS00319; A4_EXTRA; 1.
KW	Glycoprotein; Amyloid; Neuron; Transmembrane.	DR	PROSTE; PS00320; A4_INTRA; 1.
FT	NON_TER 1 1	FT	PROSTE; PS00280; BPTI_KUNITZ_1; 1.
FT	CHAIN 7 49	FT	PROSTE; PS50279; BPTI_KUNITZ_2; 1.
FT	DOMAIN <1 34	KW	Glycoprotein; Amyloid; Neuron; Transmembrane; Alternative splicing;
FT	TRANSMEM 35 58	KW	Serine protease inhibitor.
FT	DOMAIN 59 >59	FT	SIGNAL; Serine protease inhibitor.
FT	NON_TER 59 59	FT	CHAIN 18 751
SEQUENCE	59 AA: 6414 MW: F43469D488A2E12D CRC64;	FT	A4 PROTEIN.
Query Match	100.0% Score: 217; DB 1; Length: 59;	FT	BETA-AMYLOID PROTEIN (POTENTIAL).
Best Local Similarity	100.0% No. 8.e-22;	FT	EXTRACELLULAR (POTENTIAL).
Matches 42;	Conservative 0; Mismatches 0;	FT	POTENTIAL.
FT	Indels 0; Gaps 0;	FT	CYTOSOLIC (POTENTIAL).
DE	D4EFRHDSGEVHHQKLVPFAEDVGSNKGAIIGLMVGGVIA 42	FT	BPTI/KUNITZ INHIBITOR.
Qy	1 DAEFRHDSGEVHHQKLVPFAEDVGSNKGAIIGLMVGGVIA 48	FT	CLATHRIN-BINDING (BY SIMILARITY).
Db	7 DAEFRHDSGEVHHQKLVPFAEDVGSNKGAIIGLMVGGVIA 48	FT	REACTIVE BOND.
RESULT 7	A4_SAISC	STANDARD:	PRT; 751 AA.
ID-	095241; AC-	AC	RESULT 8
DT	15-Dec-1998 (Rel. 37, Created)	A4_HUMAN	SEQUENCE FROM N.A.
DT	15-Dec-1998 (Rel. 37, Last sequence update)	ID	A4_HUMAN STANDARD; PRT; 770 AA.
DT	16-Oct-2001 (Rel. 40, Last annotation update)	AC	PO5067; P09000; Q16011;
DE	"Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].	DT	PO5067; P09000; Q16011; Created
DE	APP.	DT	13-AUG-1987 (Rel. 05, Created)
GN	Saimiri sciureus (Common squirrel monkey).	DT	01-NOV-1991 (Rel. 20, Last sequence update)
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DT	16-OCT-2001 (Rel. 40, Last annotation update)
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.	DE	Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (BN-II) (APP). [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
NCBI_TaxID-9521;	[1]	DE	DE OR APP OR CVAP OR ADL.
OX		GN	Hom sapiens (Human).
RN		OS	Macaca; Metaceo; Chordata; Craniata; Vertebrata; Euteleostomi;
RP	SEQUENCE FROM N.A.	OC	Neomys; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RC	TISSUE-Liver, and Kidney;	OX	NCBI_TaxID-9606;
RX	MEDLINE=96108492; PubMed=8532114;	RN	[1]
RA	Levy E., Amorim A., Frangione B., Walker L.C.;	RP	SEQUENCE FROM N.A.
RT	"Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy."	RC	TISSUE-Brain;
RT	cerebral amyloid angiopathy.	RX	Medline=87144572; PubMed=2881207;
RL	Neurobiol. Aging 16: 805-808 (1995).	RA	Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
CC	-I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALLING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).	RA	Greschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein, -I- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).	RT	"The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor."
CC	-I- SIMILARITY: BELONGS TO THE APP FAMILY.	RL	Nature 325:733-736 (1987).
CC	-I- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.	RX	Medline=88122639; PubMed=2893289;
CC		RA	Ponte P., Gonzalez-Dewitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
CC		RA	"A new A4 amyloid mRNA, contains a domain homologous to serine proteinase inhibitors."
CC		RT	Nature 331:525-527 (1988).
CC		RL	[3]
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CC	EMBL: S81024; AD1347.1; -.	RA	Medline=89128427; PubMed=2783775;
CC	DR	RA	Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
CC	DR	RA	Cordell B.;
CC	DR	RT	"A new A4 amyloid mRNA, contains a domain homologous to serine proteinase inhibitors."
CC	DR	RL	Nature 331:525-527 (1988).
CC	DR	RN	[3]
CC	DR	RP	SEQUENCE FROM N.A.
CC	DR	RX	Medline=89128427; PubMed=2783775;
CC	DR	RA	Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,

- RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
"The Pre4 (65) precursor protein of Alzheimer's disease A4 amyloid
is encoded by 16 exons"; Nucleic Acids Res. 17:517-522(1989).
RL Nucleic Acids Res. 17:517-522(1989).
- RN SEQUENCE FROM N.A.
MEDLINE=9726807; PubMed=9108164;
RX Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
Saito M., Tsukuni S., Sakai Y.,
RA "A novel method for making nested deletions and its application for
sequencing of 300 kb region of human APP locus.";
RN Nucleic Acids Res. 25:1802-1808(1997).
[5]
RN SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX Tarzi R.E., McClatchey A.I., Lamperti E.D., Villa Komaroff L.,
Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
mRNA associated with Alzheimer's disease.";
RN Nature 331:528-530(1988).
[6]
RN SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushina Y., Shiojiri S., Ito H.,
RT "Novel precursor of Alzheimer's disease amyloid protein shows
protease inhibitory activity.";
RN Nature 331:530-532(1988).
[7]
RN SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE=87231971; PubMed=3035574;
RA Roakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
cerebrovascular and characteristic of the protease inhibitor domain of
the plaque amyloid peptides.";
RN Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
[8]
RN SEQUENCE OF 507-770 FROM N.A.
RX MEDLINE=88124954; PubMed=8933379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
disease brain: coding and noncoding regions of the fetal precursor
mRNA are expressed in the cortex.";
RN Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
[9]
RN SEQUENCE OF 672-681.
RX MEDLINE=88035004; PubMed=3312495.
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtelotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
and partial sequence of a 4,200-dalton peptide isolated from cortical
microvessels.";
RT Gene 49:1394-1401(1987).
RN [10]
RN SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasata H., Doh-Ura K., Furuya H., Sakaki Y.,
RT "Genomic organization of the human amyloid beta-protein precursor
gene.";
RT Gene 87:257-263(1990).
RN [11]
RN SEQUENCE OF 1-10 FROM N.A.
RC TISSUE-Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
encodes a 95-kDa polypeptide.";
RN [12]
RN SEQUENCE OF 18-50.
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.B., Cunningham D.P.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
- RN [13] IDENTITY OF APP WITH NEXIN-II.
RP RX MEDLINE=8384866; PubMed=2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with
the Kunits domain is protease nexin-II.";
RT Nature 341:144-147(1989).
RN [14] PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RP RX MEDLINE=90211252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.,
RT "Protease specificity of Kunits inhibitor domain of Alzheimer's
disease amyloid protein precursor.";
RT Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
RN COMPLEX WITH G(O).
RP RX MEDLINE=91188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsuuura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein in precursor complexes with brain GTP-binding
protein G(O).";
RL Nature 367:75-79(1993).
RN [16] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RP RX MEDLINE=9215582; PubMed=10201399;
RA Rossjohn J., Cappaill R., Feil S.C., Henry A., McKinstry W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.;
RT "Crystal structure of the N-terminal, growth factor-like domain of
Alzheimer amyloid precursor protein.";
RL Nat. Struct. Biol. 6:327-331(1999).
RN [17] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 287-344.
RP RX MEDLINE=91104913; PubMed=21254787;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;
RA "X-ray crystal structure of the protease inhibitor domain of
Alzheimer's amyloid beta-protein precursor.";
RL Biochemistry 29:10018-10022(1990).
RN [18] STRUCTURE BY NMR OF 289-344.
RP RX MEDLINE=22031488; PubMed=1718421;
RA Head S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kamarki M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
the Kunits-type inhibitor domain of the Alzheimer's beta-amyloid
precursor protein.";
RT Biochemistry 30:10467-10478(1991).
RN [19]
RN STRUCTURE BY NMR OF 672-699.
RP RX MEDLINE=94281210; PubMed=7516706;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of residues 1-28 of the amyloid beta-peptide.";
RT Biochemistry 33:7788-7796(1994).
RL Biochemistry 35:16094-16104(1996).
RN [20]
RN STRUCTURE BY NMR OF 696-706.
RP RX MEDLINE=9712622; PubMed=8973180;
RA Talaous J., Marcinowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide (25-35) in
membrane mimicking environment.";
RT Biochemistry 33:7788-7796(1994).
RL Biochemistry 35:16094-16104(1996).
RN [21]
RN STRUCTURE BY NMR OF 672-711.
RP RX MEDLINE=983359783; PubMed=9693002;
RA Coles M., Blacknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
environment. Is the membrane-spanning domain where we think it is?";
RT Biochemistry 37:11064-11077(1998).
RN [22]
RN STRUCTURE BY NMR OF 672-699.
RP RX MEDLINE=20400066; PubMed=10940222;

RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 site";
 RT
 RL J. Struct. Biol. 130:142-152(2000).
 RN STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=2040065; PubMed=10940221;
 RA Zhang S., Iwata K., Lachmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RT "The Alzheimer's peptide adopts a collapsed coil structure in
 water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;
 RA Dyrks T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT *Identification, transmembrane orientation and biogenesis of the
 amyloid A4 precursor of Alzheimer's disease.";
 RT
 Query 1 DAEFRHDSGYEVHKLFVFAEDVGSNKGAIIGLMVGGVIA 42
 Db : 672 DAEFRHDSGYEVHKLFVFAEDVGSNKGAIIGLMVGGVIA 713

RESULT 9
 A4_MOUSE
 ID AA_MOUSE
 STANDARD: PRT; 770 AA.
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP.
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TAXID=10030;
 RN [1] RP SEQUENCE OF 1-389 AND 365-770 FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=92096451; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 protein precursor.";
 RL Biochim. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DDJB databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the pro tease inhibitor domain of the A4 amyloid protein
 precursor of *Mus domesticus*";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]

RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92009999; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPlicing.
 RL Biochim. Biophys. Res. Commun. 158:906-912(1989).
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=2493550; PubMed=2493550;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 for the mouse homolog of Alzheimer's disease amyloid beta protein
 precursor";
 PT PRECURSOR;
 CC -I - SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I - ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPlicing.
 CC -I - TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -I - DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH XI1-ALPHA -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -I - SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -I - SIMILARITY: CONTAINS 1 BPT1/KUNITZ INHIBITOR DOMAIN.
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 CC
 CC EMBL; X59379; ; NOT_ANNOTATED_CDs.
 DR EMBL; M18373; AAA37139; 1.
 DR EMBL; X15110; CAA33280; 1.
 DR EMBL; D10603; BAA01456; 1.
 DR EMBL; M24397; AAA39929; 1.
 DR PIR; A27485; A27485.
 DR PIR; S04855; S04855.
 DR PIR; S19727; S19727.
 DR HSSP; P0567; 1AAP.
 DR MGD; MG1:88059; APP.
 DR InterPro; IPR001868; APP.
 DR InterPro; IPR002223; Kunitz_BPT1.
 DR ProDom; P00014; Kunitz_BPT1; 1.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PRO02023; AMYLOIDA4.
 DR PRINTS; PRO0155; Beta-APP.
 DR PROSITE; PS00059; BASICPTASE.
 DR PROSITE; PD000222; Kunitz_BPT1; 1.
 DR SMART; SM00131; KU; 1.
 DR Glycoprotein; Amyloid; Neurone; Transmembrane; Signal.
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723 POTENTIAL.
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.

FT DOMAIN	287	345	BPT1/KUNITZ INHIBITOR.	DR PIR; S00550; S00550.
FT SITE	759	762	CLATHRIN BINDING (BY SIMILARITY).	DR PIR; S03607; S03607.
FT DISULFID	291	341	BY SIMILARITY.	DR HSSP; P05067; IAP.
FT DISULFID	300	324	BY SIMILARITY.	DR InterPro; IPR001868; A4_APP.
FT DISULFID	316	337	BY SIMILARITY.	DR InterPro; IPR001255; Beta-APP.
FT CARBOHYD	542	542	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR InterPro; IPR00223; Kunitz_BPT1.
FT CARBOHYD	571	571	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR Pfam; PF00014; Kunitz_BPT1; 1.
FT VARSPLIC	289	289	E -> V (IN ISOFORM APP(695)).	DR Pfam; PF02177; A4_EXTRA; 1.
FT VARSPLIC	290	364	MISSING (IN ISOFORM APP(695)).	DR Pfam; PF03494; Beta_APP; 1.
FT VARSPLIC	346	380	MISSING (IN ISOFORM APP(751)).	DR PRINTS; PRO0203; AMYLOID4A.
SQ SEQUENCE	770 AA;	86752 MW;	26C50DE0890CAF7A CRC64;	DR PRINTS; PRO0759; BASICPTASE.
Query Match Best Local Similarity 92.9%; Pred. No. 3.4e-18;	Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	Score 198; DB 1; Length 770;	DR PRODOM; PRO00222; Kunitz_BPT1; 1.	
YQ 1 DAEFRHDSGYEVHQKLWFAEDVGSNKGAIIGLMGGVVIA 42			DR SMART; SM00006; A4_EXTRA; 1.	
Db 672 DAEFGHDGSGEVHQKLWFAEDVGSNKGAIIGLMGGVVIA 713			DR SMART; SM00131; KU; 1.	
RESULT 10			DR PROSITE; PS00319; A4_EXTRA; 1.	
A4_RAT	ID A4_RAT	STANDARD;	DR PROSITE; PS00320; A4_INTRA; 1.	
AC P05192;	PRT; 770 AA.		DR PROSITE; PS00280; BPT1_KUNITZ; 1.	
DT 01-AUG-1988 (Rel. 08, Created)			DR PROSITE; PS50279; BPT1_KUNITZ; 2; 1.	
DT 01-DEC-1992 (Rel. 24, Last sequence update)			KW Alternative splicing; Serine Protease inhibitor.	
DE Alzheimer's disease amyloid A4 protein homolog precursor			KW Glycoprotein; Amyloid; Neuron; Transmembrane; Signal;	
(Amyloidogenic glycoprotein) (Ag).			KW	
GN Rattus norvegicus (Rat).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			FT SIGNAL 1/17 BY SIMILARITY.	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG.	
NCBI_TaxID=10116;			FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).	
[1]			FT TRANSMEM 700 723 POTENTIAL.	
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.			FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).	
RC TISSUE=brain			FT DOMAIN 724 770 EQUIVALENT OF BETA AMYLOID PROTEIN.	
RX MEDLINE-88315583; PubMed=2300758;			FT DOMAIN 673 715 BPT1/KUNITZ INHIBITOR.	
RA Shivers B.D.; Hilbich C.; Multhaup G.; Salbaum J.M.; Beyreuther K.,			FT DOMAIN 727 345 CLATHERIN-BINDING (BY SIMILARITY).	
RT Seuburg P.H.;			FT SITE 759 762 BY SIMILARITY.	
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";			FT DISULFID 291 341 BY SIMILARITY.	
RL EMBO J. 7:1365-1370(1988).			FT DISULFID 300 324 BY SIMILARITY.	
RN [2]			FT DISULFID 316 337 BY SIMILARITY.	
RP SEQUENCE OF 289-364 FROM N.A.			FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).	
RC TISSUE=liver;			FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).	
RX MEDLINE-8913625; PubMed=2648331;			FT VARSPLIC 289 289 E -> V (IN ISOFORM APP(595)).	
RA Kang J.; Mueller-Hill B.;			FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(695)).	
RT "The sequence of the two extra exons in rat preA4.";			SO SEQUENCE 770 AA; C26C9D6BB2D929A7 CRC64;	
RL Nucleic Acids Res. 17:1130-2130(1989).			Query Match 91.2% Score 198; DB 1; Length 770;	
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.			Best Local Similarity 92.9%; Pred. No. 3.4e-18;	
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),			Matches 39; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPlicing.			QY 1 DAEFRHDSGYEVHQKLWFAEDVGSNKGAIIGLMGGVVIA 42	
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).			Db 672 DAEFRHDSGYEVHQKLWFAEDVGSNKGAIIGLMGGVVIA 42	
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.			RESULTS 11	
CC -1- SIMILARITY: CONTAINS 1 BPT1/KUNITZ INHIBITOR DOMAIN.			TR2M_AGRT4	
CC			ID TR2M_AGRT4 STANDARD;	
CC			AC P04029;	
CC			DT 23-OCT-1986 (Rel. 02, Created)	
CC			DT 15-JUN-2002 (Rel. 41, Last annotation update)	
CC			DE TRYPTOPHAN 2-monoxygenase (EC 1.13.12.3).	
CC			GN TMSI.	
CC			OS Agrobacterium tumefaciens (strain Ach5), and Agrobacterium tumefaciens.	
CC			OS Plasmid ptiAch5, and Plasmid ptiAGNC.	
CC			OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.	
CC			OC NCB_ TaxID=176298, 358;	
CC			RN [1]	
CC			SEQUENCE FROM N.A.	
CC			RC STRAIN_ACH5; PLASMD=PTIAch5;	
CC			RX MEDLINE-84207942; PubMed=6327292;	
CC			RA Gielien J.; de Beuckeleer M.; Seurinck J.; Deboeck F.; de Greve H., Lemmers M.; van Montagu M.; Scheel J., The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefaciens plasmid PTIAch5.";	
CC			RT EMBO J. 3:835-846(1984).	
CC			RN [2]	
DR X07648; CAA30488; 1;			SEQUENCE FROM N.A.	
DR X14066; CRA32229; 1;			RP	

CC	-!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.
CC	-!- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF P-HYDROXYBENZOATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEKS THAT THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.
CC	-!- SIMILARITY: STRONG, WITH ITS COUNTERPARTS FROM A. TUMEFACIENS PLASMIDS PT11595, PT11595, PT11595 AND PT116NC.
CC	-!- CAUTION: THE PLASMID PT11594 CARRIES TWO T-REGIONS, THE TA AND TB REGION, BOTH OF WHICH HAVE A FUNCTIONAL TAAM GENE, WITH LOW HOMOLOGY BETWEEN THEM.
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CC	-- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
DR	EMLB; K02554; AAA92550_1; -
DR	PIR; AA04497; Q0AGAT; Amino_Oxidase.
DR	InterPro; IPR00237; Amino_Oxidase.
DR	InterPro; IPR00064; Glycosidase.
DR	InterPro; IPR00205; NAD_binding.
DR	Pfam; PF00193; Amino_Oxidase.
DR	Pfam; PF02027; ROLB_ROLC_1.
DR	KW_Oxidoreductase; Monoxygenase; Auxin biosynthesis; Crown gall tumor; t-DNA; Plasmid.
FT	VARIANT 718 719 NR -> IQ (IN PT116NC).
FT	VARIANT 721 721 P -> A (IN PT116NC).
SEQUENCE	755 AA; 83947 MW; 9FD2B3FEA001A4D CRC64;
Qy	Query Match 28.6%; Score 62; DB 1; Length 755; Best Local Similarity 41.7%; Pred. No. 1.9; Matches 15; Conservative 6; Mismatches 9; Indels 6; Gaps 1;
Db	223 DSG----RGFPEDVPKPVAVIGAGISGLVVA 252
RESULT 13	POLG_PVYCH STANDARD; PRT; 327 AA.
ID	POLG_PVYCH
AC	P21294; AC
DT	01-MAY-1991 (Rel. 18, Created) DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE	Genome polyprotein [Contains: Nuclear inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48); Coat protein (CP)] DE (Fragment).
DE	Potato virus Y (strain Chinese isolate) (PVY); OS Potato virus Y (strain Chinese isolate) (PVY); OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; OC Potyvirus.
OX	NCBI_TaxID=12218;
RN	[1] Nucleic Acids Res. 18:5554-5554(1990). SEQUENCE FROM N.A.
RP	RP SEQUENCE FROM N.A.
STRAIN	STRAIN="PT116NC"; CC
RC	-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA) N.
RC	MEDLINE=91016851; PubMed=2216735; RX RA Zhou X.R., Fang R.X., Wang C.Q.; RT "Sequence of Agrobacterium tumefaciens biotype III auxin genes." CC CDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate)." RT
RC	Nucleic Acids Res. 18:5554-5554(1990). SEQUENCE FROM N.A.
RC	STRAIN="PT116NC"; CC
RC	-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA) N.
RC	MEDLINE=91329707; PubMed=1868204; RX RA Bonnard G., Vincent F., Otten L.; RT "Sequence of Agrobacterium tumefaciens biotype III auxin genes." CC CDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate)." RT
RC	PLANT MOLECULAR BIOLOGY 16:733-738(1991). CC
RN	[2] SEQUENCE FROM N.A.
RP	STRAIN="CG474"; CC
RA	Otten L., de Ruffray P.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RL	-!- CATALYTIC ACTIVITY: L-Tryptophan + O(2) = indole-3-acetamide + CO(2) + H(2)O.

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--

-- DR EMBL; X54054; CAA37933.1; -.

-- DR PIR; S11549; S11549;

-- DR InterPro; IPR01559; Poty_coat.

-- DR Pfam; PF00767; Poty_coat; 1.

-- KW Transf erase; RNA-directed RNA polymerase; Coat protein; Polyprotein.

-- FT NON_TER 1 1

-- FT CHAIN 61 60 NUCLEAR INCLUSION PROTEIN B.

-- FT COAT PROTEIN 327 AA; 36868 MW; 8F8355E2DB6F2F18 CRC64;

-- SQ 327 AA; Score 57; DB 1; Length 327;

-- Best Local Similarity 53.1%; Pred. No. 3.7%;

-- Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

-- QY 1 DAEFRHDSGYEVHKVQFLWFAED---VGSNK 28

-- Db 47 DDEFEELS-YEVHQK ---ANDTIDAVGDNK 72

-- OS Mycoplasma pneumoniae.

-- OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

-- OX NCBI_TaxID=104;

-- RN [1]

-- RP SEQUENCE FROM N.A.

-- RC Y226_MYCPN STANDARD; PRT; 503 AA.

-- AC P5462;

-- DT 01-NOV-1997 (Rel. 35, Created)

-- DT 16-OCT-2001 (Rel. 40, Last annotation update)

-- DE Hypothetical protein MG226 homolog (F10_of503).

-- RL MG319 OR MF517.

-- OS Mycoplasma pneumoniae.

-- OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

-- OX NCBI_TaxID=104;

-- RN [1]

-- RP SEQUENCE FROM N.A.

-- RC Y226_MYCPN 2934.2 / M129;

-- RX MEDLINE=97105885; PubMed=8948633;

-- RA Hammelreich R.; Hilbert H.; Plagens H.; Pirkl E.; Li B.-C.,

-- RA RT "Complete sequence analysis of the genome of the bacterium Mycoplasma

-- pneumoniae".

-- RL Nucleic Acids Res. 24:4420-4449(1996).

-- CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-- CC -I- SIMILARITY: TO M.GENTITALUM MG225.

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-- DR EMBL; AE00051; AAB96165.1; -.

-- DR InterPro; IPR002293; AA/rei_prmeasel.

-- DR Hypothetical protein; aa_permeases; 1.

-- KW Transmembrane protein; Transmembrane; Complete proteome.

-- FT TRANSMEM 20 40 POTENTIAL.

-- FT TRANSMEM 43 63 POTENTIAL.

-- FT TRANSMEM 106 126 POTENTIAL.

-- FT TRANSMEM 138 158 POTENTIAL.

-- FT TRANSMEM 166 186 POTENTIAL.

-- FT TRANSMEM 215 235 POTENTIAL.

-- FT TRANSMEM 249 269 POTENTIAL.

-- FT TRANSMEM 301 321 POTENTIAL.

-- FT TRANSMEM 359 379 POTENTIAL.

-- FT TRANSMEM 405 425 POTENTIAL.

-- FT TRANSMEM 443 463 POTENTIAL.

-- FT TRANSMEM 468 488 POTENTIAL.

-- SQ SEQUENCE 503 AA; 54960 MW; 4BC1BFDE036985B2 CRC64;

Query Match 26.3%; Score 57; DB 1; Length 503;
 Best Local Similarity 61.1%; Pred. No. 5.7%;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 24 VGSNKGAIIGLYVGWVI 41
 | | :| :| :| :| :| :

Db 131 VKDNGALIGLYVGFWL 148
 | | :| :| :| :| :| :

RESULT 15

SLG1_YEAST STANDARD; PRT; 378 AA.

AC P5467; SLG1_YEAST

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE SLG1 protein precursor.

GN SLG1 OR YOR008C OR UNP378.

OS Fungi; Ascomycota; Saccharomyces cerevisiae (Baker's yeast).

OC Saccharomycetidales; Saccharomyctaceae; Saccharomyces.

NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA de Bettiniere G.; Bergez-Aulio P.; Barthe C.; Louvet O.,

RA Peypouquet M.F.; Morel C.; Doignon F.; Crouzet M.,

RA Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97051599; PubMed=8896276;

RX Sterky F.; Holmberg A.; Pettersson B.; Uhlen M.;

RX "The sequence of a 30 kb fragment on the left arm of chromosome XV

-- RT from Saccharomyces cerevisiae reveals 15 open reading frames, five of

-- RT which correspond to previously identified genes."

RN Yeast 12:1091-1095(1996).

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-- CC EMBL; U34481; AAA85862.1; -.

-- DR EMBL; U43491; AAC19488.1; -.

-- DR EMBL; U74916; CAA93196.1; -.

-- DR SGD; S0005534; SLG1.

-- DR InterPro; IPR002884; WSC.

-- DR Pfam; PF01822; WSC; 1.

-- DR SMART; SM00321; WSC; 1.

-- DR Glycoprotein; Signal; SIGNAL.

-- FT CHA1_N 20 378 SIGNAL.

-- FT CARBOHYD 65 65 N-LINKED (GLCNAC, .) (POTENTIAL).

-- FT CARBOHYD 354 354 N-LINKED (GLCNAC, .) (POTENTIAL).

-- SQ SEQUENCE 378 AA; 39270 MW; EEE16AF2374CCCE3 CRC64;

-- SQ SIGNAL 1 19 POTENTIAL.

-- FT CHA1_N 20 378 SIGL.

-- FT CARBOHYD 65 65 N-LINKED (GLCNAC, .) (POTENTIAL).

-- SQ SEQUENCE 378 AA; 39270 MW; EEE16AF2374CCCE3 CRC64;

-- SQ SIGNAL 1 19 POTENTIAL.

-- FT CHA1_N 20 378 SIGL.

-- FT CARBOHYD 65 65 N-LINKED (GLCNAC, .) (POTENTIAL).

-- SQ SEQUENCE 378 AA; 39270 MW; EEE16AF2374CCCE3 CRC64;

-- SQ SIGNAL 1 19 POTENTIAL.

Query Match 26.3%; Score 57; DB 1; Length 378;

Best Local Similarity 42.4%; Pred. No. 5;

Matches 14; Conservative 5; Mismatches 5; Indels 9; Gaps 1;

DR 8 SGYVHHQKLVEPAEDVCSNKGAIGLMVGGVV 40
 | | :| :| :| :| :| :

Db 251 SGSTHKKK-----ANVGAIVGGVGGVV 274

Search completed: April 21, 2003, 12:06:47
 Job time : 14 secs

F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C;Accession: F60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X56127; PID:CAA39592_1; PID:g1896
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
 Query Match 100 %; Score 217; DB 2; Length 57;
 Best Local Similarity 100 %; Pred. No. 1e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 42 .

RESULT 4
 G60045 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X56126
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
 Query Match 100 %; Score 217; DB 2; Length 57;
 Best Local Similarity 100 %; Pred. No. 1e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 42 .

RESULT 5
 D60045 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Accession: D60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56124
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
 Query Match 100 %; Score 217; DB 2; Length 57;
 Best Local Similarity 100 %; Pred. No. 1e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 42

Db 6 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 47

RESULT 6
 A60045 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
 C;Species: Canis lupus familiaris (dog)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C;Accession: A60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 R;Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: A60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56125
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
 Query Match 100 %; Score 217; DB 2; Length 57;
 Best Local Similarity 100 %; Pred. No. 1e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 7
 B60045 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C;Species: Ursus maritimus (polar bear)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C;Accession: B60045
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 R;Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A;Reference number: A60045; MUID:92017079; PMID:1656157
 A;Accession: B60045
 A;Molecule type: mRNA
 A;Residues: 1-57 <JOH>
 A;Cross-references: EMBL:X56128; PID:92165; PID:CAA39593_1; PID:92166
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
 Query Match 100 %; Score 217; DB 2; Length 57;
 Best Local Similarity 100 %; Pred. No. 1e-21;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 8
 P00438 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C;Accession: P00438; C60045
 R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
 R;Biochem. Biophys. Res. Commun. 188, 905-911, 1992
 A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
 A;Reference number: PQ0438; MUID:93075180; PMID:1445331
 A;Accession: PQ0438
 A;Molecule type: DNA
 A;Residues: 1-82 <DAV>
 A;Cross-references: GB:M83556; GB:M83657
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 R;Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d |

Qy 1 DAEFRHDSGYEVHKLYFFAEDVGSNKGAIIGLMVGGVIA 42

A; Reference number: A60045; MUID:92017079; PMID:1656157
 A; Accession: C60045
 A; Molecule type: mRNA
 A; Residues: 12-68 <JOH>
 A; Cross-references: EMBL:X56129
 C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor; Down's syndrome
 C; Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 217; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1..6.e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 DAERFRHDSSGYEVHHQKLVFFAEDVGNSNGAIGLMVGGVIA 42
 Db 17 DAERFRHDSSGYEVHHQKLVFFAEDVGNSNGAIGLMVGGVIA 58

RESULT 9

A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C; Species: Macaca fascicularis (crab-eating macaque)
 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C; Accession: A49795
 R; Poolison, M.B.; Tolani, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A; Title: Homology of the amyloid beta protein precursor in monkey and human supports a P
 A; Reference number: A49795; MUID:91273117; PMID:1905108
 A; Accession: A49795
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1..695 <POD>
 A; Cross-references: GB:M58727; NID:9342062; PID:AAA6829..1; PMID:9342063
 C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
 C; Keywords: alternative splicing

Query Match 100.0%; Score 217; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 1..6.e-20;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DAERFRHDSSGYEVHHQKLVFFAEDVGNSNGAIGLMVGGVIA 42
 Db 597 DAERFRHDSSGYEVHHQKLVFFAEDVGNSNGAIGLMVGGVIA 638

RESULT 10

ORHIA4
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N; Alternative names: Alzheimer's disease amyloid A4 protein; coagulation factor Xta inhibitor
 N; Contains: amyloid beta protein long. Plaque form; amyloid beta protein short, vascular
 Protein precursor splice form APP(770),
 C; Species: Homo sapiens (man)
 C; Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 C; Accession: S02260; S05194; A293277; A33260; A35486; A39452; I39453; I59562; A44466B; A28583; A293278; A60805; JI0038; S06121; A60355; A50011; A38384; S29076; S32252; S32
 R; Lemaire, H.G.; Salbaum, J.M.; Multatup, G.; Kang, J.; Bayne, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res 17, 51-522, 1999
 A; Title: The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by
 A; Reference number: S02260; MUID:89128427; PMID:2783775
 A; Accession: S02260
 A; Molecule type: DNA
 A; Residues: 1-288 'V'..365-770 <LEM1>
 A; Cross-references: EMBL:X13466
 A; Note: alternative splice form APP(695)
 R; Lemaire, H.G.
 A; Reference number: S05194
 A; Accession: S05194
 A; Molecule type: DNA
 A; Residues: 1-14, 'W'..17-288, 'V'..365-770 <LEM2>
 A; Cross-references: EMBL:X13466; NID:35598; PTIN:CAA31830..1; PMID:9871360
 A; Note: alternative splice form APP(695)
 R; La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A; Residues: 687-718 <KAM>
A; Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:929611
A; Experimental source: familial Alzheimer disease family LIT
A; Note: sequence extracted from NCBI backbone (NCBIP:115316)
A; Note: this sequence has a silent mutation
R; Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Nature 325, 733-736, 1987
A; Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface protein
A; Reference number: A03134; MUID:87144572; PMID:2881207
A; Accession: A03134
A; Molecule type: mRNA
A; Residues: 1-388, 'V', 365-770 <KAN>
A; Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:928526
A; Note: alternative splice form APP(695)
R; Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A; Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and chromosomal localization of a cDNA encoding brain amyloid A; Accession: A29030
A; Molecule type: mRNA
A; Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A; Cross-references: GB:MI6765; NID:917539; PIDN:AAA51722.1; PID:g178540
A; Note: the authors translated the codon GAG for residue 647 as ASP
R; Goldgaber, D.; Lemman, M.I.; McBride, O.W.; Sarfatti, U.; Gajdusek, D.C.
Science 255, 877-880, 1987
A; Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid A; Reference number: A47584; MUID:87120328; PMID:3810169
A; Accession: A7584
A; Molecule type: mRNA
A; Residues: 674-756 'S', 758-770 <GOL>
A; Cross-references: GB:MI5533; NID:9178706; PIDN:AAA35540.1; PID:g178707
A; Experimental source: brain
R; Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, J.M.; Neve, R.; Dykens, T.; Weidemann, A.; Multhaup, G.; Lemaire, H.G.; Kang, J.; Mueller, EMBO J. 7, 949-957, 1988
A; Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the A; Reference number: A47585; MUID:87120329; PMID:2949567
A; Accession: A7585
A; Molecule type: mRNA
A; Residues: 674-703 <TAN1>
A; Cross-references: GB:MI5532; NID:9177957; PIDN:AAA1564.1; PID:g177958
R; Tanzi, R.E.; McCLatchey, A.L.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, Nature 331, 528-530, 1988
A; Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor
A; Reference number: S02638; MUID:88296437; PMID:2900137
A; Accession: S02638
A; Molecule type: mRNA
A; Residues: 672-678 <DYR>
A; Cross-references: R; Tanzi, R.E.; McCLatchey, A.L.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, Nature 331, 528-530, 1988
A; Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease
A; Reference number: S00707; MUID:88122640; PMID:2893290
A; Accession: S00707
A; Molecule type: mRNA
A; Residues: 286-344, 'I', 365-366 <PTAN2>
A; Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:929612
A; Experimental source: promyelocytic leukemia cell line HL60
A; Note: alternative splice form APP(751)
R; Ponte, P.; Gonzalez-Deshiffre, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da Costa, M.; Ito, H.
Nature 331, 525-527, 1988
A; Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitor
A; Reference number: S00925; MUID:88122639; PMID:2893289
A; Accession: S00925
A; Molecule type: mRNA
A; Residues: 1-344, 'I', 365-770 <PO2>
A; Cross-references: GB:X06983; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:928721
A; Note: alternative splice form APP(751)
R; Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A; Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A; Reference number: A38949; MUID:88122641; PMID:2893291
A; Accession: A38949
A; Molecule type: mRNA
A; Residues: 287-367 <KITP>

A; Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:929611
A; Experimental source: glioblastoma cell line
A; Note: alternative splice form APP(770)
R; Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Bartus, R.T.; Beer, B.; Ash
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A; Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three Alzheimer patients
A; Reference number: A30320
A; Accession: A30320
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 284-388, 'V', 365-770 <VIT1>
A; Accession: B30320
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 122-388, 'V', 365-770 <VIT2>
A; Accession: C30320
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 606-770 <VIT3>
R; Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A; Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A; Reference number: A31087; MUID:88124954; PMID:2893379
A; Accession: A31087
A; Molecule type: mRNA
A; Residues: 507-770 <ZAI>
A; Cross-references: GB:MI8734; NID:9178572; PIDN:AAA51726.1; PID:9178573
A; Note: the authors translated the codon GAA for residue 599 as GLY, ACC for residue 8 as Val, CGC for residue 609 as Asn, ATT for residue 610 as GLY, and GCT for residue 810 as Val
A; Note: the cited Genbank accession number, J03594, is not in release 101.0
R; Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, Query Match 100.0%; Score 217; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 1-8e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 672 DAEFRHDSGYEVHKVFFADVGNSKGAGIGLMVGVVIA 42
Qy 1 DAEFRHDSGYEVHKVFFADVGNSKGAGIGLMVGVVIA 42
Db 672 DAEFRHDSGYEVHKVFFADVGNSKGAGIGLMVGVVIA 713
RESULT 11
A; Title: Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
A; Note: proteinase nexin II
C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C; Accession: A27485; S19727; I49485
R; Yamada, T.; Sakai, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A; Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
A; Reference number: S19727; MUID:92096458; PMID:1756177
A; Accession: S19727
A; Molecule type: mRNA
A; Residues: 1-210, 'G', 212-220, 'S', 222-336, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A; Cross-references: EMBL:X59379
R; Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1991
A; Title: Positive and negative regulatory elements for the expression of the Alzheimer A; Reference number: I49485
A; Status: translated from GB/ENBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-19 <RES>

Matches 16; Conservative 5; Mismatches 9; Index 6; Gaps 1;
Qy 7 DSGYEVHQLVFFARDVGSNKGATIGLMYGGVIA 42
Db 223 DSG-----RIGFFPEDVPKVAIIAGAGISGLVVA 252

Search completed: April 21, 2003, 12:07:46
Job time : 20 secs

XX Disclosure; Fig 3; 98pp; English.

XX The inventors specifically claim transgenic mice contg. DNA encoding A42 (beta amyloid precursor protein) (AAR2030), A99 (beta-amyloid carboxy tail) (AAR20329), A695 (beta-amyloid precursor protein), A751 (precursor plus inhibitor) or A41 (protease inhibitor) (AAR20328).

CC Human fibroblast cDNA clone lambdaAPC168i4 was deposited at ATCC on July 1, 1987 and has accession No. 40347. The promoter is pref. the NSE promoter with the A751 or the A695 sequence.

XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 13; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25; Indels 0; Gaps 0;

Matches 42; Conservative 0; Mismatches 0; DE Beta/A4-amyloid peptide.

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGWVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGWVIA 42

RESULT 3
ID AAR95248
ID AAR95248 standard; peptide; 42 AA.

XX AC AAR95248;
XX DT 20 JAN 1997 (first entry)
XX DE Beta/A4-amyloid peptide.
XX KW Beta/A4-amyloid peptide; tissue plasminogen activator;
KW Alzheimer's disease; stimulation; investigation; Pathogenesis;
KW hereditary cerebral hemorrhage with amyloidosis-Dutch type;
KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;
KW hemorrhage.
XX OS Homo sapiens.
XX PN WO9615799-A1.
XX PD 30-MAY-1996.
XX DT 22-NOV-1995; 95WO-US15007.
XX PR 22-NOV-1994; 94US-0347144.
XX PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX PI Anderson S;
XX DR WPI: 1996-268332/27.
XX PT Use of agents which bind beta-amyloid peptide - for diagnosis,
PT prevention and treatment of vascular damage caused by amyloid
PT deposits, partic. in haemorrhaging and Alzheimer's disease
XX Example 1; Fig 1; 52pp; English.
XX CC To investigate the effects of beta-amyloid peptide (BAP) on
tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
CC One peptide contained 42 amino acids and corresp. to the full
length BAP (AAR5248). The other 2 peptides (AAR5249 and 50) contained
the 28 N-terminal residues of the BAP found in Alzheimer's disease
CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
(HCWA-D), respectively. In an assay to determine the effect of
CC the peptides on t-PA activation, each peptide (AAR5248, 49 and 50)
CC gave 1st order rate constant of activation (k_{app}) values of
CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for rnil
CC and fibrinogen controls. The results demonstrate that the BAP are
CC able to stimulate t-PA activity in vitro, which is significant in
CC that it provides a means for investigating and controlling the
CC pathogenesis of Alzheimer's disease, HCWA-D and cerebral amyloid
CC angiopathy related cerebral haemorrhage.
XX Sequence 42 AA;

Query Match 100.0%; Score 217; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGWVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGWVIA 42

RESULT 4
ID AAR94591

ID	AAR94591	standard; peptide; 42 AA.	PN	WO9707403-A1.
XX			XX	
AC	AAR94591;		PD	27-FEB-1997.
XX			XX	23-JUL-1997;
DT	21-AUG-1996	(first entry)	PF	96WO-US12034.
XX			XX	
DE	Alzheimer amyloid beta-protein active site sequence.		PR	16-AUG-1995;
XX			XX	95US-0515606.
KW	Beta-amyloid; Alzheimer's disease; cholinesterase; lipase; ebelactone-A; serine Protease; para-aminophenylmethanesulphonyl fluoride; inhibition; KW complex formation; alpha(1)-antichymotrypsin; Down's diseases; ageing.		(HMR) HOBCHST MARION ROUSSEL INC.	
XX			PA	Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;
OS	Synthetic.		XX	
PN	US5506097-A.		XX	WPI: 1997-165447/15.
XX			XX	DR: 1997-165447/15.
PD	09-APR-1996.	Determ. of the degree of beteA4 peptide aggregation using binding agent - used to screen cpds. for possible use in Alzheimer's disease treatment	PT	
XX			PT	
PF	24-AUG-1990:	90US-0572671.	PS	
XX			XX	This sequence represents the beta A4 peptide. The degree of aggregation of this peptide is determined using the method of the invention. The beta A4 peptide is present in the brain of Alzheimer's disease patients, but not in the brain of non-Alzheimer's disease individuals. The peptide clumps or aggregates in the brain of Alzheimer's disease patients, where it may be responsible for the destruction of normal brain cells. Once the CC clumps or aggregates form, the formulation is almost irreversible. The method of the invention comprises reacting this sequence with a binding reagent capable of binding to it only in its non aggregated state, to form an amount of a beta A4 peptide-bound reagent and an amount of protein free reagent. The amount of the beta A4 peptide, binding reagent complex is then measured. Compounds which inhibit aggregation of beta A4 peptide are potentially useful for treatment of Alzheimer's disease.
PR	10-JAN-1994;	94US-0179574.	XX	
PR	24-AUG-1990;	90US-0572671.	XX	
PR	13-JAN-1992;	92US-0819361.	XX	
PR	13-JAN-1993;	93NO-0500325.	XX	
XX			PA	(HARD) HARVARD COLLEGE.
PA	Kayyali U, Potter H;		PI	
PI	Kayyali U, Potter H;		XX	
XX			DR	WPI: 1996-200270/20.
XX			XX	Inhibiting enzymatic activity of Alzheimer amyloid beta-protein - using P-amidino:phenyl:methanesulphonyl fluoride or ebelactone A, for treatment, study and diagnosis of Alzheimer's disease, etc.
PT			PT	
PT			PT	
PS	Disclosure; Fig 1; 17pp; English.		XX	
XX			XX	
CC	This is the sequence of a fragment of the beta amyloid protein associated with Alzheimer's disease. The protein contains esterase (cholinesterase and lipase) activities based on active site similarities CC with serine proteases (see AAR94592-96). The esterase activity of the beta-amyloid protein is inhibited by the cpds. of the invention i.e. CC ebelactone A or para-aminophenylmethanesulphonyl fluoride. Inhibition CC of these activities prevents complex formation between the beta-amyloid protein and alpha(1)-antichymotrypsin, thus can be used to treat, study CC or diagnose Alzheimer's or Down's diseases or normal ageing.		XX	
CC			XX	
SQ	Sequence 42 AA:		XX	
XX			XX	
Query	Match	100.0%;	XX	Query Match
Best Local Similarity	100.0%;	Pred. No. 8.2e-25;	AC	Best Local Similarity
Matches	42;	Mismatches 0;	AC	100.0%;
		Indels 0;	AC	Score 217;
		Gaps 0;	AC	DB 18;
			AC	Length 42;
QY	1 DAEFRHDSGYEVHHQLVFFAEDGVSNKGAIIGLMVGVVIA 42		XX	Matches 42;
Db	1 DAEFRHDSGYEVHHQLVFFAEDGVSNKGAIIGLMVGVVIA 42		XX	Conservative 0;
			XX	Mismatches 0;
			XX	Indels 0;
			XX	Gaps 0;
			XX	
RESULT	5		XX	20-OCT-1998 (first entry)
AAW12828			XX	Neurotoxic beta-amyloid peptide decoy peptide #20.
ID	AAW12828	standard; peptide; 42 AA.	DE	Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;
XX			XX	aggregates; Alzheimer's disease; decoy; treatment.
AC	AAW12828;		XX	
XX			XX	
AC	AAW12828;		XX	
XX			XX	
DT	08-DEC-1997	(first entry)	XX	
XX			XX	
DE	Beta A4 peptide.		PR	29-OCT-1997;
XX			PR	97US-0960188.
KW	Beta A4 peptide; alzheimer's disease; peptide aggregation; brain; therapy; inhibitor.		PR	10-JAN-1997;
XX			XX	97US-0035847.
OS	Homo sapiens.		PA	(MASI) MASSACHUSETTS INST TECHNOLOGY.
XX			PI	Blanchard BJ, Ingram VM;
XX			XX	

PI Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;
 XX WPI; 1999-403957/34.

XX Determination of degree of aggregation of a peptide, useful for identifying therapeutic drugs for treating Alzheimer's disease

PT PT

XX Claim 1; Column 7-8; 8pp; English.

XX This invention describes a novel method for the determination of the degree of aggregation of an amyloid beta A4 peptide (1) in solution. Determination comprises: (a) incubating a sample of unaggregated (I) with Coomassie Brilliant Blue G 250 dye (III) which only binds to unaggregated (I); (b) measuring the amount of (II) bound to (I) to obtain a value (1); (c) repeating steps (a) and (b) with a second sample at a different time to obtain a second value (iii); and (d) determining the difference between (1) and (ii) which is inversely related to the degree of aggregation of (I). This method may be applied to a screen for compounds that inhibit aggregation of (I). These inhibitors may be used as therapeutic drugs to inhibit the formation of these aggregates in the brains of patients suffering from Alzheimer's disease.

XX Sequence 42 AA;

Query Match 100 %; Score 217; DB 20; Length 42;
 Best Local Similarity 100 %; Pred. No. 8.2e-25; Mismatches 0; Indels 0; Gaps 0;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKLVFAEDVGSNKGAIIGLMVGGVIA 42
 Db - 1 DAEFRHDSGYEVHKLVFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 13
 AAW29093 ID AAW29093 standard; peptide; 42 AA.
 XX AC AAW29093;
 XX DT 20-JUL-1999 (first entry)
 XX DE A-beta-binding peptide 1-42.
 XX KW Cyclosporin; A-beta peptide; conjugate; neurological disease; Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis; ALS; non-immunosuppressive; amyloid plaque formation.
 XX KW KW KW KW
 XX OS Homo sapiens.
 XX PN WO9910374-A1.
 XX PD 04-MAR-1999.
 XX PP 25-AUG-1998; 98WO-US17544.
 XX PR 26-AUG-1997; 97US-0057751.
 XX PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX PI Rich DH, Solomon ME;
 XX DR WPI; 1999-276928/23.
 XX PS Claim 5; Page 98; 129pp; English.
 XX CC New conjugates are disclosed which are of formula A-Z, in which: A is (1) a cyclosporin A analogue described in AAW29097 or (2) an FK506 binding peptide inhibitor; and Z is a polypeptide comprising 5 or more contiguous residues of A-beta peptide. The compounds are novel, chemical inducers of dimerization which are non-immunosuppressive and which are inhibitors of A-beta peptide aggregation and deposition in amyloid plaques. The adverse consequences of amyloid plaque formation can be prevented or ameliorated by sequestering the A-beta peptide in monomeric form with a conjugate which links the A-beta to cyclophilin or FKBP, therefore providing a mechanism to minimize the amount of free A-beta.

XX PA (SCIO-) SCIOS INC.
 XX PI Cordell B;
 XX DR WPI; 1999-357231/30.
 XX PT Transgenic mice useful for studying compounds potentially useful in the treatment of Alzheimer's disease
 XX Disclosure; Fig 3; 72pp; English.
 XX PS

CC available for fibril formation and deposition. The compounds can be used
 CC for the treatment of Alzheimer's disease, multiple sclerosis and
 XX amyotrophic lateral sclerosis.

SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHKLFFAEDGSNKGAIIGLMYGGVIA 42
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1 DAEFRHDSGYEVHKLFFAEDGSNKGAIIGLMYGGVIA 42

RESULT 14

AAW99585
 ID AAW99585 standard; peptide; 42 AA.
 XX
 AC AAW99585;
 XX
 DT 22-JUN-1999 (first entry)
 DE Mutant aggregating amyloid-beta peptide.
 XX
 KW Aggregation; amyloid-beta peptide; fluorescent group; detection;
 KW diagnosis; Alzheimer's disease.
 XX
 PT Yankner BA;
 PN WO9908695-A1.
 XX
 PD 25-FEB-1999.
 XX
 PP 13-AUG-1998; 98WO-US16809.
 XX
 PR 14-AUG-1997; 97US-0055660.
 XX
 PA (RECC) UNIV CALIFORNIA.
 XX
 PI Garzon-Rodriguez W, Glabe C;
 DR WPI; 1999-190112/16.
 XX
 PT New fluorescent labeled amyloid A-beta peptides
 XX
 PS Example 1; Page 21; 50pp; English.
 XX

This sequence corresponds to a mutant aggregating amyloid-beta peptide
 CC which can be covalently labelled with a fluorescent group. The detection
 CC or monitoring of an amyloid aggregate in a sample can be used to diagnose
 CC or detect a predisposition to Alzheimer's disease. The screening assays
 CC can be used to identify compounds for the treatment or amelioration of
 CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the
 CC amyloid beta peptide are also useful for exploring other aspects of
 CC amyloid structure.

SQ Sequence 42 AA;

Query Match 100.0%; Score 217; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.2e-25;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHKLFFAEDGSNKGAIIGLMYGGVIA 42
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1 DAEFRHDSGYEVHKLFFAEDGSNKGAIIGLMYGGVIA 42
 XX

RESULT 15

AAW92726
 ID AAW92726 standard; peptide; 42 AA.

